



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 197724

TO: Jane Zara
Art Unit: 1635
Location: rem/2A59/2C18
Case Serial Number: 10/636065

Friday, August 11, 2006

From: Beverly Shears
Location: Biotech-Chem Library
REM-1A54
Phone: (571)272-2528

beverly.shears@uspto.gov

Search Notes

Your queries have completed processing. You may access an electronic version via eDAN (SCORE) and /or <http://es/ScoreAccessWeb>. If the result files have been separated into two (2) or more versions, you may view additional files via the "[View version list for this application](#)" link.

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).



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ACCESS DB # 1977
PLEASE PRINT CLEAR

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 8-7-
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/636,065
Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER D)

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: ANTISENSE LAP OLIGOS

Inventors (please provide full names): KORNEJUK et al.

Earliest Priority Date: 8/7/03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

21 NA 19 Please Search Seq ID No:

22 NA 19 21

29 NA 19 — size limit to 70 NT's.

— EXACT IDENTITY needed.

may — NO INTERFERENCE SEARCH PLEASE.

THANKS.

STAFF USE ONLY

Searcher: <u>Beverly 2528</u>	Type of Search	Vendors and cost where applicable
Searcher Phone #: _____	____ NA Sequence (#)	____ STN ____ Dialog
Searcher Location: _____	____ AA Sequence (#)	____ Questel/Orbit ____ Lexis/Nexis
Date Searcher Picked Up: _____	____ Structure (#)	____ Westlaw ____ WWW/Internet
Date Completed: _____	____ Bibliographic	____ In-house sequence systems <u>CGW</u>
Searcher Prep & Review Time: _____	____ Litigation	____ Commercial ____ Oligomer ____ Score/Length
Online Time: _____	____ Fulltext	____ Interference ____ SPDI ____ Encode/Transl
	____ Other	____ Other (specify)

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 07:05:47 / Search time 221.333 Seconds
(without alignments)
598.521 Million cell updates/sec

Title: US-10-636-065-29

Perfect score: 19

Sequence: 1 cgcacglatcccttcac 19

Scoring table: IDENTITY_NUC

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5484110

Minimum DB seq length: 0
Maximum DB seq length: 70

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

1: N_Geneseq_8:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2001bs:*
7: geneseqn2002as:*
8: geneseqn2002bs:*
9: geneseqn2003as:*
10: geneseqn2003bs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	6	ABK93682 Human inh
2	19	100.0	19	14	AEA10008 Antisense
3	19	100.0	19	14	AEA10086 Antisense
4	18	94.7	23	3	AAA64903 Reverse P
5	16	84.2	29	14	AEA17843 Human IAP
6	15	78.9	19	14	ADX86146 Human IAP
7	15	78.9	19	14	ADX86613 Human IAP
8	14	73.7	19	10	ADP68184 XIAP targ
9	14	73.7	19	10	ADP68184 Human ant
10	14	73.7	19	14	ADP68262 Human ant
11	14	73.7	19	14	AEA10122 Antisense
12	14	73.7	19	14	AEA10108 Antisense
13	14	73.7	19	14	AEA09518 Antisense
14	14	73.7	19	14	AEA10267 Antisense
15	14	73.7	19	14	AEA09518 Antisense
16	13.8	72.6	33	6	ABA97854 Oligonuc
17	13.8	72.6	33	8	ACC70715 Yeast PCR
18	13.8	72.6	59	2	AAV76807 Staphyloc

19	13.8	72.6	60	14	AEB27488	AEb27488 P. radiat
20	13.4	70.5	24	2	AA053958	AA053958 Human OTC
21	13.4	70.5	37	2	AA16221	AA16221 BRYODIN 1
22	13.4	70.5	60	6	ABN37919	ABN37919 Human sp1
23	13.2	69.5	20	2	AA093159	AA093159 PCR prime
24	13.2	69.5	21	12	ADM72682	ADM72682 Human TAG
25	13.2	69.5	29	10	ADL01767	ADL01767 Tobacco t
26	13.2	69.5	42	10	ADG76422	ADG76422 Primer #4
27	13.2	69.5	42	12	ADJ21021	ADJ21021 Citrate s
28	13.2	69.5	55	12	ADQ26310	ADQ26310 Internal
29	13.2	69.5	60	12	ADQ26317	ADQ26317 Internal
30	13.2	69.5	65	16	ABN28183	ABN28183 Rat sp1ic
31	13	68.4	19	14	AEBC23674	AEBC23674 Forward P
32	12.8	67.4	22	2	AA036205	AA036205 Primer us
33	12.8	67.4	23	2	AA036207	AA036207 Primer us
34	12.8	67.4	25	9	ACI49799	ACI49799 Human mic
35	12.8	67.4	25	9	ACK16942	ACK16942 Human mic
36	12.8	67.4	25	9	ACK02223	ACK02223 Human mic
37	12.8	67.4	25	9	ACI07104	ACI07104 Human mic
38	12.8	67.4	25	10	ACF79228	ACF79228 Human Nek
39	12.8	67.4	31	14	ABN31091	ABN31091 Hog chole
40	12.8	67.4	38	11	AD051609	AD051609 Human TAG
41	12.8	67.4	38	11	AD051606	AD051606 Human TAG
42	12.8	67.4	38	15	AEF03242	AEF03242 Primer KC
43	12.8	67.4	52	4	AA165699	AA165699 Nucleotid
44	12.8	67.4	52	4	AA165700	AA165700 Nucleotid
45	12.8	67.4	52	6	AA18208	AA18208 Partial D
46	12.8	67.4	52	6	ABV73812	ABV73812 Partial s
47	12.8	67.4	52	8	ABX14804	ABX14804 Chimeric
48	12.8	67.4	52	8	ABX11364	ABX11364 DNA seqe
49	12.8	67.4	52	8	ABX11381	ABX11381 DNA seqe
50	12.8	67.4	52	10	ADD44579	ADD44579 DNA encod
51	12.8	67.4	52	10	ADD44184	ADD44184 PLC871 pl
52	12.8	67.4	52	10	ADD63596	ADD63596 Plasmid p
53	12.8	67.4	52	10	ADG27453	ADG27453 PLC871 pa
54	12.8	67.4	52	10	ACA61168	ACA61168 DNA encod
55	12.8	67.4	52	11	ADM15666	ADM15666 PLC871 pl
56	12.8	67.4	52	11	ADM15668	ADM15668 PLC871 pl
57	12.8	67.4	52	11	ADM83172	ADM83172 PLC871 pl
58	12.8	67.4	52	12	ADP89634	ADP89634 Vector pl
59	12.8	67.4	52	13	ADP60297	ADP60297 Human Igg
60	12.8	67.4	52	13	ADP47341	ADP47341 Plasmid p
61	12.8	67.4	52	14	ADX97620	ADX97620 PLC871 re
62	12.8	67.4	52	14	ADZ19096	ADZ19096 PLC871 re
63	12.8	67.4	52	14	AE81631	AE81631 PLC871 pl
64	12.8	67.4	52	14	AE804268	AE804268 Ant1-TNF
65	12.8	67.4	52	15	AEF54755	AEF54755 PLC871 pa
66	12.8	67.4	52	15	AEF07126	AEF07126 Partial n
67	12.8	67.4	52	15	AEF38563	AEF38563 PLC871 pa
68	12.8	67.4	52	15	AEF40635	AEF40635 PLC871 DN
69	12.8	67.4	70	2	AA056709	AA056709 Sequence
70	12.8	67.4	70	2	AA056707	AA056707 Sequence
71	12.6	66.3	19	14	AEA10089	AEA10089 Antisense
72	12.6	66.3	21	12	ADK97924	ADK97924 Primer of
73	12.6	66.3	30	3	AA063824	AA063824 Bovine h1
74	12.6	66.3	35	12	AD026814	AD026814 CD40 tran
75	12.6	66.3	35	12	AD026923	AD026923 CD40 vari
76	12.6	66.3	39	2	AAV72614	AAV72614 Rat Facto
77	12.6	66.3	39	2	AAZ09550	AAZ09550 Rat Facto
78	12.6	66.3	50	6	ABZ02105	ABZ02105 Human leu
79	12.6	66.3	50	12	ADP10127	ADP10127 50-mer ol
80	12.6	66.3	50	12	ADU24922	ADU24922 Retroelem
81	12.6	66.3	50	13	ADU22389	ADU22389 Human tra
82	12.6	66.3	50	13	AAA49666	AAA49666 Pig cost1
83	12.6	66.3	59	6	ABN33040	ABN33040 Human sp1
84	12.6	66.3	65	6	ABN54850	ABN54850 Mouse sp1
85	12.6	65.3	19	12	AD061052	AD061052 Ant1-HCK
86	12.4	65.3	20	14	ADZ97966	ADZ97966 Human ant
87	12.4	65.3	21	3	AA090860	AA090860 Oligonuc
88	12.4	65.3	21	3	AAZ74577	AAZ74577 Human bla
89	12.4	65.3	21	13	ADU27486	ADU27486 Knock-dow
90	12.4	65.3	21	14	ACI48718	ACI48718 FOLH1 tar
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C	92	12.4	65.3	21	14	AC148720	POLH	SIR	AC148720	POLH	SIR
	93	12.4	65.3	21	14	AC148719	POLH	SIR	AC148719	POLH	SIR
	94	12.4	65.3	21	14	AC148716	POLH	SIR	AC148716	POLH	SIR
	95	12.4	65.3	21	14	AC148715	POLH	TSR	AC148715	POLH	TSR
C	96	12.4	65.3	21	14	AC148717	POLH	SIR	AC148717	POLH	SIR
	97	12.4	65.3	24	14	ADQ98314	Human	PSR	ADQ98314	Human	PSR
	98	12.4	65.3	24	14	ADQ98073	Human	HGR	ADQ98073	Human	HGR
	99	12.4	65.3	25	9	AC161573	Human	mic	AC161573	Human	mic
C	100	12.4	65.3	25	9	AC161570	Human	mic	AC161570	Human	mic

ALIGNMENTS

RESULT 1	
ABK93682	
ABK93682	standard; DNA; 19 BP.
XX	
AC	ABK93682;
XX	
26-AUG-2002	(first entry)

Human inhibitor of apoptosis, XIAP, antisense oligonucleotide #29.

adenovirus infection; proliferative disease.
 KKM lupus erythematosus; herpes virus infection; pox virus infection;
 KKM autoimmune disorder; neurodegenerative diseases; multiple sclerosis
 KKM pancreatic cancer; embryonic development; viral pathogenesis;
 KKM cytostratic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KKM Human; ss; antisense; inhibitor of apoptosis; HAIPI, HAP2, XIAP;
 KKM

Homo sapiens

PN WO200226968-A2.

PD 04-APR-2002.

PF 27-SEP-2001; 2001WO-CA001379.

PR 28-SEP-2000; 2000US-00672717.

PA (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.

Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

WPI; 2002-479562/51.

PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.

PS Claim 8; Page 33; 135pp; English.

The invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (I) that inhibits IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, HAIAP or HAIAP2. Also included are a pharmaceutical composition comprising a mammalian IAP antisense molecule and a method of enhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, suppress or prevent proliferative diseases (e.g. ovarian cancer, adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic development, viral pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is an IAP antisense molecule of the invention.

SQ Sequence 19 BP, 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Qy 1 CGCAGGTATCTCCTTAC 19
|||
Db 1 CGCAGGTATCTCCTTAC 19

RESULT 2

ID AEA10008 standard; DNA; 19 BP.

AC AEAL0008;DT 14-JUL-2005 (first entry)

DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 29.

KW Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.

OS Homo sapiens.

XX

PN WO2005042030-A1

PD 12-MAY-2005

PF 29-OCT-2004; 2004WO-CA001900.

PR 30-OCT-2003; 2003US-0516263P.

PA (AEGE-) AEGERA THERAPEUTICS INC.

PI Lacasse E, Mcmanus D, Durkin JP;

DR WPI; 2005-366517/37.

PT Treating proliferative disease such as hepatoma, bile duct carcinoma, PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering PT antisense inhibitor of apoptosis nucleoside oligomer and chemotherapeutic PT agent.

PS Claim 6; SEQ ID NO 29; 285pp; English.

CC The invention relates to a method of treating a patient having a
CC proliferative disease, comprising administering to the patient, an
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
CC chemotherapeutic agent, in amounts that together are sufficient to treat
CC the patient. The method is useful for treating a patient having a
CC proliferative disease. The proliferative disease is cancer. A composition
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
CC human cancer cell in vivo or ex vivo, which involves contacting the cell
CC with the composition. The present sequence represents an antisense
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
CC sequence represents either T or U. There are multiple versions of this
CC sequence in the patent, the present sequence represents the sequence
CC shown in the main body of the specification.

SQ Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

Query March	100.0%	Score 19;	DB 14;	Length 19;
Best Local Similarity	100.0%	Pred. No. 5.7;		
Matches 19; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

Qy 1 CGCAGGATCTCTTCAC 19
 |||||
 Db 1 CGCAGGATCTCTTCAC 19

RESULT 3

ID AEA10086

AEAl0086 standard; DNA; 19 BP.

XX AC AEAl0086;

XX DT 14-JUL-2005 (first entry)

XX DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 107.

XX KW Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key location/Qualifiers

XX FT modified_base 1..3

XX FT /*tag= a

XX FT /mod_base= OTHER

XX FT /note= "OTHER = 2'-O-methyl X RNA"

XX FT modified_base 17..19

XX FT /*tag= b

XX FT /mod_base= OTHER

XX FT /note= "OTHER = 2'-O-methyl X RNA"

XX PN WO2005042030-A1.

XX PD 12-MAY-2005.

XX PF 29-OCT-2004; 2004MO-CA001900.

XX PR 30-OCT-2003; 2003US-0516263P.

XX PA (AEGE-) AEGERA THERAPEUTICS INC.

XX PI Lacasease E. Mcmanus D, Durkin JP;

XX PT WPI; 2005-366517/37.

XX DR

XX XX

XX PT Treating proliferative disease such as hepatoma, bile duct carcinoma,

XX PT chorloccarcinoma, seminoma and embryonal carcinoma comprises administering

XX PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic

XX PT agent.

XX PS

XX XX

XX CC The invention relates to a method of treating a patient having a

XX CC proliferative disease, comprising administering to the patient, an

XX CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a

XX CC chemotherapeutic agent, in amounts that together are sufficient to treat

XX CC the patient. The method is useful for treating a patient having a

XX CC proliferative disease. The proliferative disease is cancer. A composition

XX CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic

XX CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or

XX CC human cancer cell in vivo or ex vivo, which involves contacting the cell

XX CC with the composition. The present sequence represents an antisense

XX CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the

XX CC sequence represents either T or U. There are multiple versions of this

XX CC sequence in the patent, the present sequence represents the sequence

XX CC shown in the main body of the specification.

XX CC

XX SQ

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AA64903

ID AA64903

AA64903 standard; DNA; 23 BP.

XX AC AA64903;

XX DT 07-NOV-2000 (first entry)

XX DE Reverse PCR primer targeted to human X-linked inhibitor of apoptosis.

XX KW X-linked inhibitor of apoptosis; XIAP, hIAP, MIRA; antisense;

XX KW antiinflammatory; cytostatic; tumour; PCR primer; ss.

XX OS Homo sapiens.

XX OS

XX PN US6087173-A.

XX PD 11-JUL-2000.

XX PF 09-SEP-1999; 99US-00392580.

XX PR 09-SEP-1999; 99US-00392580.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Cowser LM, Ackermann EJ;

XX PT WPI; 2000-498201/44.

XX DR

XX XX

XX PT Antisense compound useful for research reagents, diagnostics, prophylaxis

XX PT and for treating disorders associated with X-linked inhibitor of

XX PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.

XX XX

XX PS

XX XX

XX CC The present invention relates to antisense oligonucleotides designed to

XX CC inhibit expression of the human X-linked inhibitor of apoptosis. Modified

XX CC phosphorothioate 2'-MOE oligonucleotides are more effective inhibitors

XX CC than unmodified oligonucleotides. The oligonucleotides may be used to

XX CC inhibit X-linked inhibitor of apoptosis expression in cells and tissues

XX CC in vitro. The oligonucleotides are also useful for treating animals or

XX CC humans, prone to a disease associated with X-linked inhibitor of

XX CC apoptosis. The oligonucleotides may also be used prophylactically to

XX CC prevent infection, inflammation or tumour formation. Inhibition was

XX CC measured by comparing the level of X-linked inhibitor of apoptosis mRNA

XX CC to that of GAPDH. The present sequence is the reverse PCR primer used in

XX CC RT-PCR to measure X-linked inhibitor of apoptosis mRNA

XX SQ

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RESULT 5

ID AEA17843/c

AEAl7843 standard; DNA; 29 BP.

XX AC AEAl7843;

XX DT 14-JUL-2005 (first entry)

XX DE Human IAP-specific inhibitor oligonucleotide - SEQ ID 37.

XX KW inhibitor of apoptosis protein; gene silencing; apoptosis stimulation;

XX KW cancer; cytostatic; ss; IAP.

XX OS Homo sapiens.

XX OS

XX PN

XX PD

XX PF

XX PR

XX PA

XX PI

XX PT

XX DR

XX XX

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

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XX PT

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XX PT

RESULT 4

```

FH Key Location/Qualifiers
FT misc_difference 2
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FT /note= "N = T or U"
FT misc_difference 5
FT /*tag= b
FT /note= "N = T or U"
FT misc_difference 8
FT /*tag= c
FT /note= "N = T or U"
FT misc_difference 17
FT /*tag= d
FT /note= "N = T or U"
FT misc_difference 22
FT /*tag= e
FT /note= "N = T or U"
FT misc_difference 27
FT /*tag= f
FT /note= "N = T or U"
XX WO2005042558-A1.
XX
XX 12-MAY-2005.
XX
XX 29-OCT-2004; 2004WO-CA001902.
XX
XX 30-OCT-2003; 2003US-0516192P.
XX
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Lacase E, Mcmannus D;
XX
XX WPI; 2005-346849/35.
XX
XX New pure nucleobase oligomer comprising a duplex comprising at least
XX eight but no more than 30 consecutive nucleobases corresponding to XIAP,
XX hIAP-1 or hIAP-2, useful in preparing a composition for treating cancer.
XX
XX Claim 9; SEQ ID NO 37; 112bp; English.
XX
XX The invention comprises oligonucleotides which are capable of educing the
XX expression of X-linked inhibitor of apoptosis protein (XIAP), hIAP-1 or
XX hIAP-2. The oligonucleotides of the invention are useful for the
XX treatment of proliferative disease (e.g. cancer). The present DNA
XX sequence represents an IAP-specific inhibitory oligonucleotide of the
XX invention.
XX
XX Sequence 29 BP; 7 A; 5 C; 11 G; 0 T; 0 U; 6 Other;
XX
XX Query Match 84.2%; Score 16; DB 14; Length 29;
XX Best Local Similarity 84.2%; Pred. No. 2.2e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 CGCAGCGTATCTCTCTTAC 19
XX |||||
XX 25 CGCNCGGTNTCTCTTCTTNC 7
XX
XX RESULT 6
XX ADX86146/c
XX ID ADX86146 standard; RNA; 19 BP.
XX
XX ADX86146;
XX
XX 05-MAY-2005 (first entry)
XX
XX XIAP targeting siRNA SEQ ID NO 17.
XX
XX de; primer; short interfering RNA; siRNA;
XX X-linked inhibitor of apoptosis protein; XIAP; RNA interference; RNAi;
XX cyostatic; cancer; gene silencing.
XX
XX OS Synthetic.
```

```

XX
XX WO2005014811-A2.
XX
XX 17-FEB-2005.
XX
XX 06-AUG-2004; 2004WO-US025589.
XX
XX 08-AUG-2003; 2003US-0493561P.
XX 23-OCT-2003; 2003US-00693059.
XX 24-NOV-2003; 2003US-00720448.
XX 03-DEC-2003; 2003US-00727780.
XX 14-JAN-2004; 2004US-00757803.
XX 10-FEB-2004; 2004US-0543480P.
XX 13-FEB-2004; 2004US-00780447.
XX 16-APR-2004; 2004US-00826966.
XX 30-APR-2004; 2004WO-US013456.
XX 24-MAY-2004; 2004WO-US016390.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Chowitra BM;
XX
XX WPI; 2005-163247/17.
XX
XX New chemically synthesized double stranded short interfering nucleic acid
XX that directs cleavage of an X-linked inhibitor of apoptosis protein
XX (XIAP) RNA via RNA interference, useful in preparing a composition for
XX treating cancer.
XX
XX Claim 33; SEQ ID NO 17; 202bp; English.
XX
XX This invention describes novel chemically synthesized double stranded
XX short interfering nucleic acid (siRNA) molecules which direct cleavage of
XX a X-linked inhibitor of apoptosis protein (XIAP) RNA via RNA interference
XX (RNAi), where each strand of the siRNA molecule is about 18-23
XX nucleotides in length and one strand of the siRNA molecule comprises
XX nucleotide sequence having sufficient complementarity to the XIAP RNA.
XX The siRNA molecules can be used to make a cyostatic composition
XX comprising the siRNA molecule in a carrier or diluent. The sense and
XX antisense strands are connected via a linker molecule. The pyrimidine
XX nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides.
XX The purine nucleotides in the sense region are 2'-deoxy purine
XX nucleotides and the pyrimidine nucleotides are 2'-deoxy-2'-fluoro
XX pyrimidine nucleotides. The fragment comprising the sense region includes
XX a terminal cap moiety at a 5'-end, a 3'-end, or both of the 5' and 3',
XX ends of the fragment comprising the sense region. The terminal cap moiety
XX is an inverted deoxy abasic moiety. The pyrimidine nucleotides of the
XX antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the
XX purine nucleotides are 2'-O-methyl purine nucleotides. The purine
XX nucleotides present in the antisense region comprise 2'-deoxy- purine
XX nucleotides. The antisense region comprises a phosphorothioate
XX internucleotide linkage at the 3' end of the antisense region. The
XX antisense region comprises a glyceryl modification at a 3' end of the
XX antisense region. About 19 nucleotides of each fragment of the siRNA
XX molecule are base-paired to the complementary nucleotides of the other
XX fragment of the siRNA. The 5'-end of the fragment comprising the
XX antisense region optionally includes a phosphate group. The XIAP RNA
XX comprises Genbank Accession No. NM_001157. The chemically synthesized
XX double stranded short interfering nucleic acid (siRNA) molecule is useful
XX in preparing a composition for treating cancer. ADX86130-ADX87180
XX represent siRNA molecules which are used in RNA interference mediated
XX inhibition of XIAP gene expression.
XX
XX Sequence 19 BP; 6 A; 3 C; 7 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 78.9%; Score 15; DB 14; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 7.1e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 5 CGGTATCTCTCTTAC 19
XX |||||
XX 19 CGGTATCTCTCTTAC 5
```

RESULT 7
AD86613
ID AD86613 standard; RNA; 19 BP.
AC AD86613;
XX
XX
DT 05-MAY-2005 (first entry)
DE XIAP targeting siRNA SEQ ID NO 484.
XX
XX
KM ds; primer; short interfering RNA; siRNA;
KM X-linked inhibitor of apoptosis protein; XIAP; RNA interference; RNAi;
KM cytosolic; cancer; gene silencing.
XX
OS Synthetic.
XX
PN MO2005014811-A2.
PD
PD 17-FEB-2005.
XX
PF 06-AUG-2004; 2004WO-US025589.
XX
XX 08-AUG-2003; 2003US-0493561P.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
PI Mcswigen J, Chowira BM;
XX
XX WPI; 2005-163247/17.
XX
PT New chemically synthesized double stranded short interfering nucleic acid
PT that directs cleavage of an X-linked inhibitor of apoptosis protein
PT (XIAP) RNA via RNA interference, useful in preparing a composition for
PT treating cancer.
XX
XX
PS Claim 33; SEQ ID NO 484; 202pp; English.
XX
XX This invention describes novel chemically synthesized double stranded
CC short interfering nucleic acid (siRNA) molecules which direct cleavage of
CC a X-linked inhibitor of apoptosis protein (XIAP) RNA via RNA interference
CC (RNAi), where each strand of the siRNA molecule is about 18-23
CC nucleotides in length and one strand of the siRNA molecule comprises
CC nucleotide sequence having sufficient complementarity to the XIAP RNA.
CC The siRNA molecule can be used to make a cytostatic composition
CC comprising the siRNA molecule in a carrier or diluent. The sense and
CC antisense strands are connected via a linker molecule. The sense and
CC nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides.
CC The purine nucleotides in the sense region are 2'-deoxy purine
CC nucleotides. The pyrimidine nucleotides are 2'-deoxy-2'-fluoro
CC pyrimidine nucleotides. The fragment comprising the sense region includes
CC a terminal cap moiety at a 5'-end, a 3'-end, or both of the 5' and 3'
CC ends of the fragment comprising the sense region. The terminal cap moiety
CC is an inverted deoxy abasic moiety. The pyrimidine nucleotides of the
CC antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the
CC purine nucleotides are 2'-O-methyl purine nucleotides. The purine
CC nucleotides present in the antisense region comprise 2'-deoxy- purine
CC nucleotides. The antisense region comprises a phosphorothioate
CC internucleotide linkage at the 3' end of the antisense region. The
CC antisense region comprises a glyceryl modification at a 3' end of the
CC antisense region. About 19 nucleotides of each fragment of the siRNA
CC molecule are base-paired to the complementary nucleotides of the other
CC fragment of the siRNA. The 5'-end of the fragment comprising the
CC antisense region optionally includes a phosphate group. The XIAP RNA

CC comprises Genbank Accession No. NM 001167. The chemically synthesized
CC double stranded short interfering nucleic acid (siRNA) molecule is useful
CC in preparing a composition for treating cancer. AD86130-AD87180
CC represent siRNA molecules which are used in RNA interference mediated
CC inhibition of XIAP gene expression.
XX
XX
SQ Sequence 19 BP; 3 A; 7 C; 3 G; 0 T; 6 U; 0 Other;
Query Match 78.9%; Score 15; DB 14; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.1e+02;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Oy 5 CGGATCTCCTTCAC 19
Db 1 CGGUAUCCUUCAC 15
RESULT 8
AD86184
ID AD86184 standard; DNA; 19 BP.
AC AD86184;
XX
XX
DT 12-FEB-2004 (first entry)
DE
XX
XX Human antisense XIAP nucleobase oligomer SEQ ID NO:29.
XX
XX nucleobase oligomer; inhibitor-of apoptosis inhibitor; IAP inhibitor;
KM cytosolic; antisense therapy; apoptosis enhancer; cancer;
KM lymphoproliferative disorder; leukaemia; myelodysplastic syndrome;
KM polycythemia vera; lymphoma; Hodgkin's disease;
KM Waldenstrom's macroglobulinemia; breast cancer; basal cell carcinoma;
KM lung carcinoma; melanoma; retinoblastoma; human; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX
PH Key Location/Qualifiers
FT misc_feature 1..19
FT /*tag= a
FT /note= "N = T or U where each nucleobase may be part of a
FT ribonucleotide, deoxyribonucleotide, or nucleotide
FT analogue"
XX
XX
PN MO2003080638-A2.
XX
XX
XX 02-OCT-2003.
PD
XX 27-MAR-2003; 2003WO-1B001670.
PF
XX 27-MAR-2002; 2002US-0367853P.
PR
XX (AEGE-) AEGERA THERAPEUTICS INC.
PA
XX
XX
PI Lacasease E, Mcmannus D, Durkin JP;
XX
XX WPI; 2003-779241/73.
DR
XX
XX
PT New nucleobase oligomers that inhibit expression of inhibitor of
PT apoptosis gene, useful for treating cancer and other lymphoproliferative
PT disorders by inducing apoptosis.
XX
XX
PS Claim 54; SEQ ID NO 29; 259pp; English.
XX
XX The present invention describes a substantially pure nucleobase oligomer
CC (I) of up to 30 nucleobases in length or comprising eleven DNA residues
CC flanked on each side by four 2'-O-methyl RNA residues that inhibits the
CC expression of an inhibitor-of apoptosis (IAP) in the cell. Also
CC described: (1) a pharmaceutical composition (II) comprising (I) and a
CC carrier; (2) a catalytic RNA molecule (III) capable of cleaving XIAP,
CC HIAP1, or HIAP2 mRNA; (3) an expression vector (IV) comprising a nucleic
CC acid encoding one or more (III) positioned for expression in a mammalian
CC cell; (4) a double-stranded RNA molecule (IV) consisting of 21-29

CC nucleobases, comprising at least eight consecutive nucleobases
CC corresponding to a sequence comprising 19 nucleotides, as given in
CC specification; (5) a double-stranded hairpin RNA molecule (V) consisting
CC of 50-70 nucleobases, comprising a first domain of 21-29 nucleobases that
CC comprise at least eight consecutive nucleobases corresponding to a
CC sequence fully defined in the specification, comprising, e.g. 19
CC nucleotides, and a second domain complementary to the first domain, and a
CC loop domain situated between the first and the second domains such that
CC the first domain and the second domain are capable of duplexing to form
CC the double-stranded hairpin RNA molecule; and (6) an expression vector
CC (VI) comprising a nucleic acid molecule encoding the double stranded RNA
CC molecule positioned for expression in a mammalian cell. (I) has
CC cytoskeletal activity, and can be used in antisense therapy. (I) is useful
CC for enhancing the apoptosis of a cell in an animal, preferably human
CC where (I) inhibits the expression of an IAP in the cell. (I) is also
CC useful for treating an animal having a cancer or lymphoproliferative
CC disorder. The cancer includes acute leukaemia, acute lymphocytic
CC leukaemia, acute myelocytic leukaemia, acute myeloblastic leukaemia,
CC acute promyelocytic leukaemia, acute myelomonocytic leukaemia, acute
CC monocytic leukaemia, acute erythroleukaemia, chronic leukaemia, chronic
CC myelocytic leukaemia, myelodysplastic syndrome, chronic lymphocytic
CC leukaemia, polycythemia vera, lymphoma, Hodgkin's disease, Waldenstrom's
CC macroglobulinemia, breast cancer, basal cell carcinoma, lung carcinoma,
CC melanoma and retinoblastoma. The present sequence is used in the
CC exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;
Query Match 73.7%; Score 14; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 1 CGACGGTATCTCTTCAC 19
Db 1 CGACGGNANNCNNCAC 19
RESULT 9
ADFe8262
ID ADF68262 standard; DNA; 19 BP.
XX
AC ADF68262;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human antisense IAP nucleobase oligomer SEQ ID NO:107.
XX
XX nucleobase oligomer; inhibitor-of apoptosis inhibitor; IAP inhibitor;
XX cytoskeletal; antisense therapy; apoptosis enhancer; cancer;
XX lymphoproliferative disorder; leukaemia; myelodysplastic syndrome;
XX polycythemia vera; lymphoma; Hodgkin's disease;
XX Waldenstrom's macroglobulinemia; breast cancer; basal cell carcinoma;
XX lung carcinoma; melanoma; retinoblastoma; human; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_feature 1..19
FT /*tag= a
FT /note= "N = T or U where each nucleobase may be part of a
FT ribonucleotide, deoxyribonucleotide, or nucleotide
FT analogue"
XX
XX PN WO2003080638-A2.
XX
XX PD 02-OCT-2003.
XX
XX PF 27-MAR-2003; 2003WO-IB001670.
XX
XX PR 27-MAR-2002; 2002US-0367853P.
XX
XX PA (AEGE-) AEGERA THERAPEUTICS INC.

XX
XX Lacase E, Mcmanus D, Durkin JP;
PI
XX WPI; 2003-779241/73.
XX
DR
XX
XX
PT New nucleobase oligomers that inhibit expression of inhibitor of
PT apoptosis gene, useful for treating cancer and other lymphoproliferative
PT disorders by inducing apoptosis.
XX
PS Claim 54; SEQ ID NO 107; 259pp; English.
XX
XX The present invention describes a substantially pure nucleobase oligomer
XX (I) of up to 30 nucleobases in length or comprising eleven DNA residues
XX flanked on each side by four 2'-O-methyl RNA residues that inhibits the
XX expression of an inhibitor-of apoptosis (IAP) in the cell. Also
XX described: (1) a pharmaceutical composition (II) comprising (I) and a
XX carrier; (2) a catalytic RNA molecule (III) capable of cleaving XIAP,
XX HIAP1, or HIAP2 mRNA; (3) an expression vector (IV) comprising a nucleic
XX acid encoding one or more (III) positioned for expression in a mammalian
XX cell; (4) a double-stranded RNA molecule (IV) consisting of 21-29
XX nucleobases, comprising at least eight consecutive nucleobases
XX corresponding to a sequence comprising 19 nucleotides, as given in
XX specification; (5) a double-stranded hairpin RNA molecule (V) consisting
XX of 50-70 nucleobases, comprising a first domain of 21-29 nucleobases that
XX comprise at least eight consecutive nucleobases corresponding to a
XX sequence fully defined in the specification, comprising, e.g. 19
XX nucleotides, and a second domain complementary to the first domain, and a
XX loop domain situated between the first and the second domains such that
XX the first domain and the second domain are capable of duplexing to form
XX the double-stranded hairpin RNA molecule; and (6) an expression vector
XX (VI) comprising a nucleic acid molecule encoding the double stranded RNA
XX molecule positioned for expression in a mammalian cell. (I) has
XX cytoskeletal activity, and can be used in antisense therapy. (I) is useful
XX for enhancing the apoptosis of a cell in an animal, preferably human
XX where (I) inhibits the expression of an IAP in the cell. (I) is also
XX useful for treating an animal having a cancer or lymphoproliferative
XX disorder. The cancer includes acute leukaemia, acute lymphocytic
XX leukaemia, acute myelocytic leukaemia, acute myeloblastic leukaemia,
XX acute promyelocytic leukaemia, acute myelomonocytic leukaemia, acute
XX monocytic leukaemia, acute erythroleukaemia, chronic leukaemia, chronic
XX myelocytic leukaemia, myelodysplastic syndrome, chronic lymphocytic
XX leukaemia, polycythemia vera, lymphoma, Hodgkin's disease, Waldenstrom's
XX macroglobulinemia, breast cancer, basal cell carcinoma, lung carcinoma,
XX melanoma and retinoblastoma. The present sequence is used in the
XX exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;
Query Match 73.7%; Score 14; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 1 CGACGGTATCTCTTCAC 19
Db 1 CGACGGNANNCNNCAC 19
RESULT 10
AEA10122
ID AEA10122 standard; DNA; 19 BP.
XX
XX AEA10122;
XX
DT 14-JUL-2005 (first entry)
XX
XX Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 143.
DE
XX
XX Cytoskeletal; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH

```
FT modified_base 1..4
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER = 2'-O-methyl X RNA"
FT modified_base 16..19
FT /tag= b
FT /mod_base= OTHER
FT /note= "OTHER = 2'-O-methyl X RNA"
XX WO2005042030-A1.
XX 12-MAY-2005.
XX 29-OCT-2004; 2004WO-CA001900.
XX 30-OCT-2003; 2003US-0516263P.
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX Lacase E, Mcmanus D, Durkin JP;
XX WPI; 2005-366517/37.
XX
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering
XX antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
XX agent.
XX
XX Claim 6; SEQ ID NO 143; 285bp; English.
XX
XX The invention relates to a method of treating a patient having a
XX proliferative disease, comprising administering to the patient, an
XX antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
XX chemotherapeutic agent, in amounts that together are sufficient to treat
XX the patient. The method is useful for treating a patient having a
XX proliferative disease. The proliferative disease is cancer. A composition
XX comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
XX agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
XX human cancer cell in vivo or ex vivo, which involves contacting the cell
XX with the composition. The present sequence represents an antisense
XX inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
XX sequence represents either T or U. There are multiple versions of this
XX sequence in the patent, the present sequence represents the sequence
XX shown in the main body of the specification.
XX
XX Sequence 19 BP; 4 A; 6 C; 3 G; 4 T; 2 U; 0 Other;
SQ
Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.4e+03;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 GGTATCTCCTTCAC 19
DB 1 GGTATCTCCTTCAC 14
RESULT 11
AEA10076
ID AEA10076 standard; DNA; 19 BP.
XX
XX AEA10076;
XX
XX 14-JUL-2005 (first entry)
XX
XX Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 97.
XX
XX Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..2
```

```
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER = 2'-O-methyl X RNA"
FT modified_base 18..19
FT /tag= b
FT /mod_base= OTHER
FT /note= "OTHER = 2'-O-methyl X RNA"
XX WO2005042030-A1.
XX 12-MAY-2005.
XX 29-OCT-2004; 2004WO-CA001900.
XX 30-OCT-2003; 2003US-0516263P.
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX Lacase E, Mcmanus D, Durkin JP;
XX WPI; 2005-366517/37.
XX
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering
XX antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
XX agent.
XX
XX Claim 6; SEQ ID NO 97; 285bp; English.
XX
XX The invention relates to a method of treating a patient having a
XX proliferative disease, comprising administering to the patient, an
XX antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
XX chemotherapeutic agent, in amounts that together are sufficient to treat
XX the patient. The method is useful for treating a patient having a
XX proliferative disease. The proliferative disease is cancer. A composition
XX comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
XX agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
XX human cancer cell in vivo or ex vivo, which involves contacting the cell
XX with the composition. The present sequence represents an antisense
XX inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
XX sequence represents either T or U. There are multiple versions of this
XX sequence in the patent, the present sequence represents the sequence
XX shown in the main body of the specification.
XX
XX Sequence 19 BP; 4 A; 6 C; 3 G; 5 T; 1 U; 0 Other;
SQ
Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GGTATCTCCTTCAC 19
DB 1 GGTATCTCCTTCAC 14
RESULT 12
AEA10108
ID AEA10108 standard; DNA; 19 BP.
XX
XX AEA10108;
XX
XX 14-JUL-2005 (first entry)
XX
XX Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 129.
XX
XX Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX WO2005042030-A1.
XX 12-MAY-2005.
```

XX 29-OCT-2004; 2004MO-CA001900.
XX 30-OCT-2003; 2003US-0516263P.
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX Lacasease E, Mcmanus D, Durkin JP;
XX WPI; 2005-366517/37.
XX
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering
XX antisenase inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
XX agent.
XX
XX Example 1; SEQ ID NO 129; 285pp; English.
XX
XX The invention relates to a method of treating a patient having a
XX proliferative disease, comprising administering to the patient, an
XX antisenase inhibitor of apoptosis (IAP) nucleobase oligomer and a
XX chemotherapeutic agent, in amounts that together are sufficient to treat
XX the patient. The method is useful for treating a patient having a
XX proliferative disease. The proliferative disease is cancer. A composition
XX comprising an antisenase IAP nucleobase oligomer and a chemotherapeutic
XX agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
XX human cancer cell in vivo or ex vivo, which involves contacting the cell
XX with the composition. The present sequence represents an antisenase
XX inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
XX sequence represents either T or U. There are multiple versions of this
XX shown in the main body of the specification.
XX
SQ Sequence 19 BP; 4 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
XX
Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 GGATCTCCTTCAC 19
DB 1 GGATCTCCTTCAC 14
XX
RESULT 13
AEA09518
ID AEA09518 standard; DNA; 19 BP.
XX
AC AEA09518;
XX
DT 14-JUL-2005 (first entry)
XX
DE Antisenase inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 29.
XX
XX Cytostatic; neoplasm; cancer; Antisenase; apoptosis inhibitor; ss.
XX
XX Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..19
FT /tag= a
FT /note= "The residues represented by N are either T or U"
XX
XX
XX WO2005042030-A1.
XX
XX 12-MAY-2005.
XX
XX 29-OCT-2004; 2004MO-CA001900.
XX
XX 30-OCT-2003; 2003US-0516263P.
XX
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX

XX Lacasease E, Mcmanus D, Durkin JP;
XX WPI; 2005-366517/37.
XX
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering
XX antisenase inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
XX agent.
XX
XX Claim 6; SEQ ID NO 29; 285pp; English.
XX
XX The invention relates to a method of treating a patient having a
XX proliferative disease, comprising administering to the patient, an
XX antisenase inhibitor of apoptosis (IAP) nucleobase oligomer and a
XX chemotherapeutic agent, in amounts that together are sufficient to treat
XX the patient. The method is useful for treating a patient having a
XX proliferative disease. The proliferative disease is cancer. A composition
XX comprising an antisenase IAP nucleobase oligomer and a chemotherapeutic
XX agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
XX human cancer cell in vivo or ex vivo, which involves contacting the cell
XX with the composition. The present sequence represents an antisenase
XX inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
XX sequence represents either T or U. There are multiple versions of this
XX shown in the sequence listing.
XX
SQ Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;
XX
Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 1 CGCAGGATCTCCTTCAC 19
DB 1 CGCAGGATCTCCTTCAC 19
XX
RESULT 14
AEA10267
ID AEA10267 standard; DNA; 19 BP.
XX
AC AEA10267;
XX
DT 14-JUL-2005 (first entry)
XX
DE Antisenase inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 289.
XX
XX Cytostatic; neoplasm; cancer; Antisenase; apoptosis inhibitor; ss.
XX
XX Homo sapiens.
XX
OS Synthetic.
XX
PN WO2005042030-A1.
XX
PD 12-MAY-2005.
XX
PP 29-OCT-2004; 2004MO-CA001900.
XX
PR 30-OCT-2003; 2003US-0516263P.
XX
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Lacasease E, Mcmanus D, Durkin JP;
XX
XX WPI; 2005-366517/37.
XX
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering
XX antisenase inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
XX agent.
XX
XX Claim 6; SEQ ID NO 289; 285pp; English.
XX
XX

XX The invention relates to a method of treating a patient having a
CC proliferative disease, comprising administering to the patient, an
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
CC chemotherapeutic agent, in amounts that together are sufficient to treat
CC the patient. The method is useful for treating a patient having a
CC proliferative disease. The proliferative disease is cancer. A composition
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
CC human cancer cell in vivo or ex vivo, which involves contacting the cell
CC with the composition. The present sequence represents an antisense
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
CC sequence represents either T or U. There are multiple versions of this
CC sequence in the patent, the present sequence represents the sequence
CC shown in the main body of the specification.

SQ Sequence 19 BP; 4 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGATCTCTCTTAC 19
|||
1 GGATCTCTCTTAC 14

Db 1 GGATCTCTCTTAC 14

RESULT 15
AEA09596
ID AEA09596 standard; DNA; 19 BP.
XX AEA09596;
AC
XX 14-JUL-2005 (first entry)
DT
XX
DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 107.
XX
XX Cytostratic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
KW
XX Homo sapiens.
OS
XX Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..19
FT /*tag= a
FT /note= "The residues represented by N are either T or U"
XX
XX MO2005042030-A1.
PN
XX
PD 12-MAY-2005.
XX
XX 29-OCT-2004; 2004MO-CA001900.
PF
XX
XX 30-OCT-2003; 2003US-0516263P.
PR
XX
XX (AEGE-) AEGERA THERAPEUTICS INC.
PA
XX
XX Lacasease E, Mcmanus D, Durkin JP;
PI
XX
XX WPI; 2005-366517/37.
DR
XX
XX
PT Treating proliferative disease such as hepatoma, bile duct carcinoma,
PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
PT agent.
XX
XX
XX Example 1; SEQ ID NO 107; 2855pp; English.
PS
XX
CC The invention relates to a method of treating a patient having a
CC proliferative disease, comprising administering to the patient, an
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
CC chemotherapeutic agent, in amounts that together are sufficient to treat
CC the patient. The method is useful for treating a patient having a

CC proliferative disease. The proliferative disease is cancer. A composition
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
CC human cancer cell in vivo or ex vivo, which involves contacting the cell
CC with the composition. The present sequence represents an antisense
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
CC sequence represents either T or U. There are multiple versions of this
CC sequence in the patent, the present sequence represents the sequence
CC shown in the sequence listing.

SQ Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;

Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTAC 19
|||
1 CGCAGCGTATCTCTTAC 19

Db 1 CGCAGCGTATCTCTTAC 19

RESULT 16
ABA97854/c
ID ABA97854 standard; DNA; 33 BP.
XX
XX ABA97854;
AC
XX
XX 10-APR-2002 (first entry)
DT
XX
DE Oligonucleotide MEL1-anti.
XX
XX Drug; cell wall; GPI anchor protein; ss.
KW
XX
XX Synthetic.
OS
XX
XX WO200183733-A1.
PN
XX
PD 08-NOV-2001.
XX
XX 26-APR-2001; 2001WO-JP003630.
PF
XX
XX 01-MAY-2000; 2000JP-00132041.
PR
XX
XX (DAUC) DAITCHI PHARM CO LTD.
PA
XX
XX Kitamura A, Someya K, Nakajima R;
PI
XX
XX WPI; 2002-097496/13.
DR
XX
XX
PT Screening for drugs that act on cell walls, involves culturing
PT microorganisms with a reporter protein acting as a GPI anchor protein in
PT their cell walls.
XX
XX
XX Disclosure; Page 13; 44pp; Japanese.
PS
XX
XX The invention relates to screening for drugs that act on cell walls,
CC comprising culturing microorganisms with a reporter protein acting as a
CC GPI anchor protein in their cell walls in the presence of the test
CC substance and assaying the amount of reporter protein produced in the
CC culture. The present sequence is that of an oligonucleotide useful to the
CC invention
XX
XX
SQ Sequence 33 BP; 10 A; 7 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 6; Length 33;
Best Local Similarity 88.2%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTAC 17
|||
26 CTCACGGTATCGCCTTC 10

Db 26 CTCACGGTATCGCCTTC 10

```
RESULT 17
ACCT0715/c
ID ACC70715 standard; DNA; 33 BP.
XX
XX ACC70715;
AC
XX
XX 20-NOV-2003 (first entry)
XX
XX Yeast PCR primer MEL1-ant1.
XX
XX Yeast; antifungal; cell wall; fungal infection; PCR; primer; ss.
XX
XX Saccharomyces cerevisiae.
XX
XX WO2003035898-A1.
XX
XX 01-MAY-2003.
XX
XX 22-OCT-2002; 2002WO-0P010932.
XX
XX 22-OCT-2001; 2001JP-00323293.
XX
XX (DAUC ) DAICHI PHARM CO LTD.
XX
XX Kitamura A, Nakajima R;
XX
XX WPI; 2003-430423/40.
XX
XX Screening drugs acting on cell wall based on reporter protein as GPI
XX anchor protein with analysis of its derived sugar chain, useful in
XX judging action points of drugs particularly in developing antifungal
XX agents.
XX
XX Example 1; Page 15; 51pp; Japanese.
XX
XX The present invention relates to a method for screening drugs which act
XX on cell walls. The method comprises culturing a microorganism immobilised
XX on its cell wall with a reporter protein as a GPI anchor protein, in the
XX presence of a test drug, analysing a receptor-originated sugar chain in
XX the liquid culture medium, and presuming the action point of the cell
XX wall-acting drug based on the data of the sugar chain thus obtained. The
XX method is useful for judging action points of drugs particularly in
XX developing cell-wall inhibitors for treatment of deep-site fungal
XX infection. The present sequence is a PCR primer used in an example from
XX the invention
XX
XX Sequence 33 BP; 10 A; 7 C; 11 G; 5 T; 0 U; 0 Other;
SQ
Query Match 72.6%; Score 13.8; DB 8; Length 33;
Best Local Similarity 88.2%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CGCAGCGTATCTCCTTC 17
DB 26 CTCACGCGTATCGCCTTC 10
RESULT 18
AAV76807
ID AAV76807 standard; DNA; 59 BP.
XX
XX AAV76807;
AC
XX
XX 16-MAR-1999 (first entry)
XX
XX Staphylococcus aureus contig SEQ ID #3496.
XX
XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
XX skin infection; surgical wound infection; scalded skin syndrome;
XX toxic shock syndrome; ds.
XX
XX Staphylococcus aureus.
OS
```

```
XX
XX EP766519-A2.
XX
XX 30-JUL-1997.
XX
XX 07-JAN-1997; 97EP-00100117.
XX
XX 05-JAN-1996; 96US-0009861P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX
XX WPI; 1997-374922/35.
XX
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
XX stored on computer readable medium and used in the production of anti-
XX S. aureus vaccines.
XX
XX Claim 1; Page 2254-2255; 3271pp; English.
XX
XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences
XX of the invention. The DNA sequences are recorded on a computer readable
XX medium, preferably selected from a floppy or hard disk, random access
XX memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
XX the S. aureus DNA sequences allows putative functions to be assigned so
XX that protein-encoding or regulatory regions of commercial, therapeutic or
XX industrial importance can be obtained. Specifically, sequences which are
XX likely to encode antigens have been identified and these polypeptides can
XX be used in a vaccine composition against S. aureus infection. The
XX polypeptides can also be used in a kit for the immunodetection of
XX S. aureus in a sample. S. aureus is implicated in numerous human diseases,
XX including cellulitis, eyelid infections, food poisoning, osteomyelitis,
XX skin and surgical wound infections, scalded skin syndrome, toxic shock
XX syndrome, etc. Organisms transformed with the DNA sequences can be used
XX for recombinant production of the polypeptides. The new DNA sequences
XX (and their fragments) are useful as primers or probes for isolating
XX homologues of any of the S. aureus DNA sequences contained on the computer
XX readable medium
XX
XX Sequence 59 BP; 19 A; 12 C; 8 G; 20 T; 0 U; 0 Other;
SQ
Query Match 72.6%; Score 13.8; DB 2; Length 59;
Best Local Similarity 88.2%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CGCAGCGTATCTCCTTC 17
DB 14 CGCAGCGAATTTCTTC 30
RESULT 19
AEB27488
ID AEB27488 standard; DNA; 60 BP.
XX
XX AEB27488;
AC
XX
XX 22-SEP-2005 (first entry)
XX
XX P. radiata cell cycle gene microarray oligo SEQ ID NO 649.
XX
XX plant protectant; fungicide; plant growth regulant; gene therapy;
XX cell cycle; gene expression; plant; transgenic plant; microarray; wood;
XX ss.
XX
XX Pinus radiata.
XX
XX WO2005065339-A2.
XX
XX 21-JUL-2005.
XX
XX 30-DEC-2004; 2004WO-US043804.
XX
```

PR 30-DEC-2003; 2003US-0533036P.
XX (ARBO-) ARBOGEN LLC.
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Forster RL, Connert MB, Emerson SJ, Grigor MR, Higgins CM,
PI Lund ST, Magnus A, Kodrzycki RJ;
XX WPI; 2005-506765/51.
XX
PT New polynucleotide encoding a plant cell cycle protein, useful for
PT modifying plant development and altering plant phenotype.
XX
XX
PS Claim 43; SEQ ID NO 649; 499pp; English.
XX
CC The invention describes an isolated polynucleotide comprising: (1) a
CC sequence of SEQ ID NOS: 1-237 or their conservative variants; (11) a
CC sequence encoding the catalytic or substrate-binding domain of a
CC polypeptide of SEQ ID NOS: 261-497, where the polynucleotide encodes a
CC polypeptide having the activity of the polypeptide of SEQ ID NOS: 261-497
CC ; or (111) a nucleic acid sequence of SEQ ID NOS: 471-657. Also described
CC are: (1) a DNA construct comprising at least one polynucleotide having
CC the sequence of SEQ ID NOS: 1-237 or their conservative variants; (2) a
CC plant cell transformed with the DNA construct of (1); (3) a transgenic
CC plant comprising the plant cell of (2); (4) a method of making a
CC transformed plant; (5) a wood or a wood pulp obtained from a transgenic
CC tree which has been transformed with the DNA construct of (1); (6) a
CC method of making wood or wood pulp; (7) an isolated polypeptide
CC comprising an amino acid sequence encoded by the new isolated
CC polynucleotide or comprising any of the amino acid sequences of SEQ ID
CC NOS: 261-497; (8) a method of altering a plant phenotype of a plant; (9)
CC a method of correlating gene expression in two different samples; (10) a
CC method of correlating the possession of a plant phenotype to the level of
CC gene expression in the plant of one or more genes; (11) a method of
CC correlating gene expression to a stage of the cell cycle; (12) a
CC combination, for detecting expression of one or more genes, comprising
CC two or more oligonucleotides, where each oligonucleotide is capable of
CC hybridizing to a nucleic acid sequence of SEQ ID NOS: 1-237 or to gene
CC product encoded by a nucleic acid sequence of SEQ ID NOS: 1-237; (13) a
CC microarray comprising the combination of (12) provided on a solid
CC support, where each of the two or more oligonucleotides occupies a unique
CC location on the solid support; (14) a method for detecting one or more
CC genes in a sample; (15) a method for detecting one or more nucleic acid
CC sequences encoded by one or more genes in a sample; and (16) a kit, for
CC detecting gene expression, comprising the microarray of (13) together
CC with one or more buffers or reagents for a nucleotide hybridization
CC reaction. The polynucleotides, polypeptides, DNA construct, composition,
CC and methods are useful for modifying plant development and altering plant
CC phenotype. This sequence represents an oligonucleotide used in the
CC creation of a microarray for detection of cell cycle genes.
XX
SQ Sequence 60 BP; 18 A; 13 C; 9 G; 20 T; 0 U; 0 Other;
QY
Query Match 72.6%; Score 13.8; DB 14; Length 60;
Best Local Similarity 88.2%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 3 CACGGTATCTCCTTCAC 19
24 CACTGTATCTCCTTCAC 40
RESULT 20
AAQ53958
ID AAQ53958 standard; DNA; 24 BP.
XX
XX AAQ53958;
XX
XX
DT 03-AUG-1995 (first entry)
DE Human OTC gene antisense primer, binds to bases 260-283.
XX
XX Human; OTC; identification; mutation; amplify; PCR; diagnosis;

KW fluorescence-label; primer; electrophores; genetic disease;
KW single stranded conformation polymorphism; SSCP; detection; ss.
XX
XX Synthetic.
XX
XX JP05317048-A.
XX
XX
PD 03-DEC-1993.
XX
XX
XX 30-SEP-1992; 92JP-00286605.
XX
XX 30-SEP-1991; 91JP-00280835.
XX
XX (SHIO) SHIONOGI & CO LTD.
XX (MATSU) MATSUDA I.
XX WPI; 1994-011017/02.
XX
XX
PT Gene mutation identification for genetic disease diagnosis - includes
PT specific gene or fragment amplification by polymerase chain reaction
PT using fluorescence-labelled primer and electrophoresis.
XX
XX
PS Disclosure; Page 11; 14pp; Japanese.
XX
CC The sequences given in AAQ53956-78 are primers which were used in the
CC method of the invention to detect mutations in the human OTC gene. The
CC gene is amplified by PCR using a fluorescence-labelled primer and the
CC amplified gene or fragment is electrophoresed by single stranded
CC conformation polymorphism (SSCP) and detecting the mutated gene via the
CC primer. This method can be used to detect the presence of mutation in a
CC gene with a precision equal to or higher than that of RFL labelling
CC methods. This method may be used in the diagnosis of genetic disease
XX
SQ Sequence 24 BP; 7 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
QY
Query Match 70.5%; Score 13.4; DB 2; Length 24;
Best Local Similarity 93.3%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 3 CACGGTATCTCCTTC 17
10 CACTGTATCTCCTTC 24
RESULT 21
AAT16221
ID AAT16221 standard; cDNA; 37 BP.
XX
XX AAT16221;
XX
XX
DT 11-JUL-1996 (first entry)
XX
XX
DE Bryodin 1 PCR primer 4.
XX
XX
KW Bryodin 1; ribosome-inactivating protein; ligand; toxin; immunotoxin;
KW cytotoxin; cancer; Bryonia dioica; primer; PCR;
KW polymerase chain reaction; ss.
XX
XX Synthetic.
XX
XX CA2148724-A.
XX
XX
PD 18-NOV-1995.
XX
XX
XX 05-MAY-1995; 95CA-02148724.
XX
XX
XX 17-MAY-1994; 94US-00245754.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Siegal1 CB;
XX
XX WPI; 1996-077793/09.

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XX  Oligo:nucleotide encoding ribosome-inactivating bryodin 1 from Bryonia
PT  dioica - inhibits protein synthesis in vitro and is useful as ligand or
PT  toxin conjugates or fusion proteins to selectively kill, e.g. cancer
PT  cells.
XX
XX  Example 4; Page 24; 46pp; English.
XX
XX  Following PCR amplification of cDNA coding for bryodin 1 (see also
CC  AAT16208) and insertion of the product into vector pET22b, the PelB
CC  leader sequence contained in the resulting intermediate vector was
CC  removed by digesting with XbaI and NcoI, and ligating the resulting 6106
CC  bp fragment with an oligoduplex formed by the annealing of primers 3
CC  (AAT16220) and 4 (AAT16221). The resulting plasmid, pSE313.0, was used for
CC  transformation of E. coli BL21. Recombinant bryodin 1 (see also AAR92481)
CC  was produced that had potent protein synthesis inhibitory activity (ED50
CC  = 3-4 µM).
XX
SQ  Sequence 37 BP; 13 A; 6 C; 3 G; 15 T; 0 U; 0 Other;
XX
Query Match          70.5%; Score 13.4; DB 2; Length 37;
Best Local Similarity 93.3%; Pred. No. 5.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY  3 CACGGTATCTCCTTC 17
    |||||
DB  1 CATGGTATCTCCTTC 15
XX
RESULT 22
ABN37919/C
ID  ABN37919 standard; DNA; 60 BP.
XX
AC  ABN37919;
XX
DT  15-JUL-2002 (first entry)
XX
DE  Human spliced transcript detection oligonucleotide SEQ ID NO:10667.
XX
KW  Human; mouse; rat; splice transcript; detection; RNA transcript;
KM  splice variant; transcriptome; oligonucleotide library; ss.
XX
OS  Homo sapiens.
XX
WO200210449-A2.
XX
PD  07-FEB-2002.
XX
PF  20-JUL-2001; 2001WO-IB001903.
XX
PR  28-JUL-2000; 2000US-0221607P.
XX
PR  02-MAY-2001; 2001US-0287724P.
XX
PA  (COMP-) COMPUGEN INC.
XX
PI  Shoshan A, Maeserman A, Mintz E, Mintz I, Faigler S;
XX
WPI; 2002-257383/30.
XX
DR  2002-257383/30.
XX
PT  New oligonucleotide libraries comprising oligonucleotides which
PT  selectively hybridize to mRNAs transcribed from a transcription unit of a
PT  genome, useful for detecting tissue-, pathology-, and developmental-
PT  specific genes.
XX
XX  Example 1; SEQ ID NO 10667; 47pp; English.
XX
XX  The present invention describes oligonucleotide libraries for detecting
CC  messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
CC  transcriptome comprises messenger RNAs transcribed from multiple
CC  transcription units that populate a genome. The library comprises several
CC  oligonucleotides, each capable of hybridising selectively to a set of
CC  messenger RNAs transcribed from a given transcription unit of the genome,
CC  which encodes one or more messenger RNA splice variants. The

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CC  oligonucleotide libraries are useful for detecting mRNAs from a
CC  biological sample, in expression profiling studies, in qualitatively or
CC  quantitatively characterizing the corresponding transcriptome, and in
CC  detecting RNA transcripts and splice variants of human or animal
CC  transcriptomes. The libraries may also be used as specialised mini
CC  libraries to detect transcripts of a sub-transcriptome under a particular
CC  biological or pathological state, and so allowing the detection of tissue
CC  - and pathology-specific genes such as those genes only expressed in
CC  specific tissue under a specific pathological condition; to detect
CC  developmental specific genes; and to detect RNA transcripts and splice
CC  variants of a transcriptome of a patient suffering from a particular
CC  disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC  rats, humans and mice, which are used in the exemplification of the
CC  present invention. N.B. The sequence data for this patent did not form
CC  part of the printed specification, but was obtained in electronic format
CC  directly from WIGO at ftp.wigo.int/pub/published_pct_sequences
XX
SQ  Sequence 60 BP; 21 A; 10 C; 20 G; 9 T; 0 U; 0 Other;
XX
Query Match          70.5%; Score 13.4; DB 6; Length 60;
Best Local Similarity 93.3%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY  5 CGGTATCTCCTTCAC 19
    |||||
DB  27 CTGTATCTCCTTCAC 13
XX
RESULT 23
AAK93159/C
ID  AAK93159 standard; DNA; 20 BP.
XX
AC  AAK93159;
XX
DT  13-SEP-1999 (first entry)
XX
DE  PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW  Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KM  sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW  neutralising epitope; PCR primer; ss.
XX
OS  Synthetic.
XX
OS  Chlamydia pneumoniae.
XX
PN  WO92927105-A2.
XX
XX  03-JUN-1999.
XX
PD  20-NOV-1998; 98WO-IB001890.
XX
PF  21-NOV-1997; 97FR-00014673.
XX
PR  04-NOV-1998; 98US-0107078P.
XX
PA  (GEST ) GENSET.
XX
PI  Griffiths R;
XX
WPI; 1999-357842/30.
XX
DR  1999-357842/30.
XX
PT  Genome sequence of Chlamydia pneumoniae.
XX
PS  Page 1568; Disclosure; 1912pp; English.
XX
XX  AAK1991-X97517 represent PCR primers used to amplify open reading frames
CC  and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC  (see AAK91990). C. pneumoniae causes respiratory disease such as
CC  pneumonia and bronchitis and is thought to be a contributing factor in
CC  heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC  nodosum or pharyngitis. The polypeptides encoded by the open reading
CC  frames of the C. pneumoniae genome (see AAY34584 - AAY35879) can be used
CC  in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC  nucleotide sequences can also be used as immunogenic compositions,

```

CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae
 XX
 SQ Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 2; Length 20;
 Best Local Similarity 83.3%; Pred. No. 6.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCACGATCTCTCTTCA 19
 |||||
 Db 18 GGACGATCTCTCTTCA 1

RESULT 24
 ADM72682/c
 ID ADM72682 standard; RNA; 21 BP.
 XX
 AC ADM72682;
 XX

DT 17-JUN-2004 (first entry)
 XX
 DE Human TASK120(1) siRNA antisense oligo.

XX TASK; tumour-associated kinase; cytostatic; tumour;
 KM cell proliferative disorder; cancer; transgenic;
 KM chromosome identification; tissue typing; TASK120; siRNA;
 KM small interfering RNA; ds.
 XX

OS Synthetic.

XX WO2004024063-A2.

XX 25-MAR-2004.

XX 05-SEP-2003; 2003WO-US027886.

XX 11-SEP-2002; 2002US-0410166P.

XX (GETH) GENENTECH INC.

XX Davis DP, Desauvage FJ, Wood WT, Zhang Z;
 XX

XX WPI; 2004-282984/26.

PT New tumor-associated kinase nucleic acids and polypeptides, useful as
 PT hybridization probes for isolating full length TASK DNA, for generating
 PT transgenic animals, in chromosome identification, or for tissue typing.
 XX

PS Example 4; Page 92; 140pp; English.

CC The invention relates to tumour-associated kinase (TASK) polypeptides
 CC (II) and encoding polynucleotides. An antibody, oligopeptide (siRNA) or
 CC organic molecule that binds to (II) is useful for treating a mammal
 CC having a tumour comprising cells expressing (II). Antagonists of TASK are
 CC useful for treating or preventing a cell proliferative disorder (e.g.
 CC cancer) associated with increased expression or activity of (II). The
 CC TASK polynucleotides and polypeptides may be used as hybridization probes
 CC for isolating full length TASK DNA, for generating transgenic animals, in
 CC chromosome identification, or for tissue typing. Sequences ADM72681-
 CC ADM72686 represent small interfering RNA (siRNA) oligonucleotides
 CC specific for TASK120.
 XX

XX Sequence 21 BP; 4 A; 3 C; 10 G; 2 T; 2 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 12; Length 21;
 Best Local Similarity 83.3%; Pred. No. 6.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGATCTCTCTTCA 18
 |||||
 Db 19 CGCAGGATCTCTCTTCA 2

RESULT 25
 ADL01767
 ID ADL01767 standard; DNA; 29 BP.
 XX
 AC ADL01767;
 XX

DT 06-MAY-2004 (first entry)
 XX

DE Tobacco translationally controlled tumour protein, TCTP, PCR primer #3.
 XX
 XX ss; PCR; transgenic; plant; translationally controlled tumour protein;
 KM agronomic phenotype; tobacco; TCTP; primer.
 XX

OS Nicotiana tabacum.

XX US2003131384-A1.

XX 10-JUL-2003.

XX 16-JAN-2003; 2003US-00345599.

XX 22-SEP-2000; 2000KR-00055727.

XX 15-DEC-2000; 2000US-00737300.

XX (KANG/) KANG J.

XX (YUN/) YUN J.

XX (SONG/) SONG P.

XX (PARK/) PARK C.

XX Kang J, Yun J, Song P, Park C;
 XX

XX WPI; 2003-635877/60.

XX New transgenic plant cell or its progeny transformed with a
 XX PT translationally controlled tumor protein gene, useful for producing
 XX PT higher plants exhibiting several desirable agronomic phenotypes.
 XX

PS Disclosure; Page 6; 19pp; English.
 XX
 XX The invention relates to a transgenic plant cell or its progeny
 CC transformed with and expressing a gene encoding the translationally
 CC controlled tumor protein. The methods and compositions of the present
 CC invention are useful for providing a new tool to accelerate the growth
 CC rate of higher plants exhibiting several desirable agronomic phenotypes
 CC by transforming cells of higher plants with the TCTP gene. The present
 CC sequence represents a tobacco translationally controlled tumour protein,
 CC TCTP, PCR primer.
 XX

PS Sequence 29 BP; 6 A; 10 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 10; Length 29;
 Best Local Similarity 83.3%; Pred. No. 6.5e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGATCTCTCTTCA 18
 |||||
 Db 9 CGCAGGATCTCTCTTCA 26

RESULT 26

ADG76422
 ID ADG76422 standard; DNA; 42 BP.
 XX

XX ADG76422;
 AC

DT 11-MAR-2004 (first entry)
 XX

DE Primer #4 of the invention.
 XX

XX Gram-negative bacterium; Entner-Doudoroff pathway;
 KM 6-phosphogluconate dehydratase; EDP;
 KM 2-keto-3-deoxy-6-phosphogluconate aldolase; EDA; primer; ss.

XX Synthetic.
OS
XX
PN EP1352966-A2.
XX
PD 15-OCT-2003.
XX
PF 26-MAR-2003; 2003EP-00006936.
XX
PR 27-MAR-2002; 2002JP-00088668.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Hara Y, Izui H, Asano T, Watanabe Y, Nakamatsu T;
XX
DR WPI; 2003-815163/77.
XX
PT Production of L-amino acids in Gram-negative bacteria, useful
PT particularly for making glutamic acid, by increasing activity of Entner-
PT Doudoroff pathway enzymes.
XX
PS Disclosure; SEQ ID NO 4; 18pp; English.
XX
CC The present invention relates to the production of L-amino acids by
CC culturing a Gram-negative bacterium that contains the Entner-Doudoroff
CC pathway and has been modified so that activity of 6-phosphogluconate
CC dehydratase (EDD) and/or 2-keto-3-deoxy-6-phosphogluconate aldolase (EDA)
CC are increased. The method is specifically used to produce L-glutamic
CC acid. The present sequence represents a primer of the invention.
XX
SQ Sequence 42 BP; 11 A; 13 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 10; Length 42;
Best Local Similarity 83.3%; Pred. No. 6.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CGCAGCGTATCTCCTTCA 18
|||
2 CGCAGCATATCCCTTCA 19

RESULT 27
AD121021
ID AD121021 standard; DNA; 42 BP.

XX
AC AD121021;
XX
DT 22-APR-2004 (first entry)
XX

XX Citrate synthase (CS) promoter primer seq id 4.

XX L-amino acid production; Entner-Doudoroff pathway;
KM 6-phosphogluconate dehydratase activity;
KM 2-keto-3-deoxy-6-phosphogluconate aldolase activity;
KM Entner-Doudoroff pathway; PCR; primer; ss; citrate synthase; CS;
KM promoter.
XX

OS Corynebacterium glutamicum.

PN US2003219882-A1.

PD 27-NOV-2003.

PF 26-MAR-2003; 2003US-00396488.

PR 26-MAR-2003; 2003US-00396488.

PA (AJIN) AJINOMOTO CO INC.

XX Hara Y, Izui H, Asano T, Watanabe Y, Nakamatsu T;
XX WPI; 2004-212658/20.
XX

PT Production of L-amino acid comprises culturing microorganism, which is
PT Gram-negative bacterium having Entner-Doudoroff pathway and which has
PT been modified so that specific activities are enhanced.
XX

PS Example; SEQ ID NO 4; 12pp; English.

XX The invention describes a method of L-amino acid production comprising
CC culturing a microorganism having an ability to produce an L-amino acid in
CC a medium. The microorganism is a Gram-negative bacterium having the
CC Entner-Doudoroff pathway and which has been modified so that 6-
CC phosphogluconate dehydratase activity or 2-keto-3-deoxy-6-
CC phosphogluconate aldolase activity, or activities of both are enhanced.
CC The method is useful for producing an L-amino acid, e.g. L-glutamic acid,
CC L-arginine, L-glutamine, L-proline, L-leucine, L-isoleucine, L-valine, or
CC L-alanine. The method improves productivity of L-amino acids in bacteria
CC from a viewpoint different from known techniques. This sequence
CC represents a primer used in the isolation of Brevibacterium
CC lactofermentum citrate synthase (CS) promoter used in the creation of an
CC Entner-Doudoroff pathway enhanced strain of Enterobacter agglomerans.
XX

SQ Sequence 42 BP; 11 A; 13 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 12; Length 42;
Best Local Similarity 83.3%; Pred. No. 6.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CGCAGCGTATCTCCTTCA 18
|||
2 CGCAGCATATCCCTTCA 19

RESULT 28
ADQ26310
ID ADQ26310 standard; DNA; 55 BP.

XX
AC ADQ26310;
XX
DT 23-SEP-2004 (first entry)
XX

DE Internal primer for siRNA expression construct M.

XX Tetracycline; operator; RNA interference; gene silencing; promoter;
KM gene therapy; short interfering RNA; siRNA; PCR; primer; ss.
XX
OS Escherichia coli.
XX

PN WO2004056964-A2.

PD 08-JUL-2004.

PF 18-DEC-2003; 2003WO-US040548.

PR 18-DEC-2002; 2002US-0434856P.
PR 28-AUG-2003; 2003US-0499313P.

PA (GENP-) GENPATH PHARM INC.

XX
PI Winston W, O'hagan RC, Heyer J, Rideout W, Etemad-Moghadam B;
XX WPI; 2004-500295/47.
XX

PT New nucleic acid construct comprising a coding sequence for a small
PT interfering RNA molecule linked operably to a mammalian or viral
PT promoter, useful for treating gene-mediated diseases, such as cancer.
XX

PS Example; SEQ ID NO 42; 58pp; English.

XX The present sequence is that of an internal primer used to insert a
CC tetracycline operator sequence ADQ26299 into a double-stranded siRNA
CC expression construct ADQ26303 designed for inducible RNA interference of
CC luciferase gene expression. The invention relates to recombinant vectors
CC containing inducible systems for expressing dsRNA molecules that
CC interfere with expression of target genes, including disease-related

CC genes (e.g. cancer-related genes such as oncogenes and tumour suppressor
CC genes). A claimed nucleic acid construct comprises a coding sequence for
CC a siRNA molecule operably linked to a mammalian or viral promoter (e.g.
CC the U6 promoter), in which the part of the nucleotide region between the
CC proximal sequence element and the transcription initiation site of the
CC promoter is replaced with an operator sequence (e.g. a tetracycline
CC operator) controlled by a small molecule.
XX
SQ Sequence 55 BP; 21 A; 10 C; 11 G; 13 T; 0 U; 0 Other;
Query Match 69.5%; Score 13.2; DB 12; Length 55;
Best Local Similarity 83.3%; Pred. No. 7e+03; 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GCACGGTATCTCTTCAC 19
2 GCACGGTATCTCTTCAC 19
Db 2 GCACGGTATCTCTTCAC 19
RESULT 29
ADQ26317/c
ID ADQ26317 standard; DNA; 60 BP.
XX
XX ADQ26317;
AC
XX
XX 23-SEP-2004 (first entry)
XX
XX Internal primer for siRNA expression construct M.
DE
XX
XX Tetracycline; operator; RNA interference; gene silencing; promoter;
KM gene therapy; short interfering RNA; siRNA; PCR; primer; ss.
XX
XX Escherichia coli.
OS
XX
XX WO2004056964-A2.
PN
XX
XX 08-JUL-2004.
PD
XX
XX 18-DEC-2003; 2003MO-US040548.
PF
XX
XX 18-DEC-2002; 2002US-0434856P.
PR
XX
XX 28-AUG-2003; 2003US-0499313P.
XX
XX (GENP-) GENPATH PHARM INC.
PA
XX
XX Winston W, O'hagan RC, Heyer J, Rideout W, Etemad-Moghadam B;
PI
XX
XX WPI; 2004-500295/47.
DR
XX
XX New nucleic acid construct comprising a coding sequence for a small
PT interfering RNA molecule linked operably to a mammalian or viral
PT promoter, useful for treating gene-mediated diseases, such as cancer.
XX
XX Example; SEQ ID NO 49; 58bp; English.
XX
XX The present sequence is that of an internal primer used to insert a
CC tetracycline operator sequence ADQ26299 into a double-stranded siRNA
CC expression construct ADQ26303 designed for inducible RNA interference of
CC luciferase gene expression. The invention relates to recombinant vectors
CC containing inducible systems for expressing dsRNA molecules that
CC interfere with expression of target genes, including disease-related
CC genes (e.g. cancer-related genes such as oncogenes and tumour suppressor
CC genes). A claimed nucleic acid construct comprises a coding sequence for
CC a siRNA molecule operably linked to a mammalian or viral promoter (e.g.
CC the U6 promoter), in which the part of the nucleotide region between the
CC proximal sequence element and the transcription initiation site of the
CC promoter is replaced with an operator sequence (e.g. a tetracycline
CC operator) controlled by a small molecule.
XX
XX
SQ Sequence 60 BP; 15 A; 16 C; 12 G; 17 T; 0 U; 0 Other;
Query Match 69.5%; Score 13.2; DB 12; Length 60;
Best Local Similarity 83.3%; Pred. No. 7.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GCACGGTATCTCTTCAC 19
2 GCACGGTATCTCTTCAC 19
Db 39 GCACGGTATCTCTTCAC 22
RESULT 30
ABN28183
ID ABN28183 standard; DNA; 65 BP.
XX
XX ABN28183;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Rat spliced transcript detection oligonucleotide SEQ ID NO:931.
DE
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Rattus norvegicus.
OS
XX
XX WO200210449-A2.
PN
XX
XX 07-FEB-2002.
PD
XX
XX 20-JUL-2001; 2001MO-IB001903.
PF
XX
XX 28-JUL-2000; 2000US-0221607P.
PR
XX
XX 02-MAY-2001; 2001US-0287724P.
XX
XX (COMP-) COMPUGEN INC.
PA
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI
XX
XX WPI; 2002-257383/30.
DR
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX Example 1; SEQ ID NO 931; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27255 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at fcp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 65 BP; 14 A; 24 C; 13 G; 14 T; 0 U; 0 Other;
Query Match 69.5%; Score 13.2; DB 6; Length 65;
Best Local Similarity 83.3%; Pred. No. 7.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AAK36207
ID AAK36207 standard; DNA; 23 BP.
XX
AC AAK36207;
XX
DT 16-JUL-1999 (first entry)
XX
DE Primer used for sequencing of the wheat Rht gene.
XX
KM Rht gene; homologue: Triticum aestivum; wheat; growth inhibition;
KM antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KM paclobutrazol; sequencing primer; ss.
XX
OS Synthetic.
XX
PN WO9909174-A1.
XX
PD 25-FEB-1999.
XX
PF 07-AUG-1998; 98WO-GB002383.
XX
PR 13-AUG-1997; 97GB-00017192.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Harberd NP, Richards DE, Peng J;
XX
DR WPI; 1999-181040/15.
XX
XX
XX New Triticum aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype.
XX
PS Claim 50; Page 51; 88pp; English.
XX
XX The specification describes polypeptides encoded by the Rht gene (and its
CC homologues) that, when expressed in Triticum aestivum, inhibit growth of
CC the plant. This growth inhibition is antagonised by gibberellin. The
CC products can be used to provide Rht expression in plants, conferring a
CC dwarf phenotype on a plant which is correctable by treatment with
CC gibberellin. In addition, the products can be used to produce Rht mutant
CC plants which are dwarfed compared with wild-type, the dwarfing being
CC gibberellin-insensitive. Taller plants may be made by knocking out Rht or
CC the relevant homologue gene in the plant of interest. Plants may be made
CC which are resistant to compounds which inhibit gibberellin biosynthesis,
CC such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis
CC inhibitor to keep weeds dwarf but let crop plants grow tall. Primers
CC AAK36199-X36233 were used in the sequencing of the Rht gene, in the
CC course of the invention
XX
SQ Sequence 23 BP; 5 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 67.4%; Score 12.8; DB 2; Length 23;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 ACGGTATCTCTTCAC 19
DB 4 AGGTTATCTCTTCAC 19
RESULT 34
ACI49799/C
ID ACI49799 standard; DNA; 25 BP.
XX
AC ACI49799;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 49790.
XX
KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; diallelic marker; polymorphism; human;

KM cross-species comparison.
XX
XX Homo sapiens.
OS
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFEX-) APEVETRIX INC.
XX
XX Miltmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 49790; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation. In Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 67.4%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 ACGGTATCTCTTCAC 19
DB 22 ACGGTATCTCTTCAC 7
RESULT 35
ACK16942/C
ID ACK16942 standard; DNA; 25 BP.
XX
AC ACK16942;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 116923.
XX
KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; diallelic marker; polymorphism; human;
KM cross-species comparison.
XX

OS Homo sapiens.
XX US2003104410-A1.
XX
XX 05-JUN-2003.
PD
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFRY-) AFRYMETRIX INC.
XX
PI Mitmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 116923; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 11 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 67.4%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 ACGGATCTCCTTCAC 19
DB 20 ACGGATCTCCTTC 5
RESULT 36
ACIO2223/C
ID ACGO2223 standard; DNA; 25 BP.
XX
XX ACGO2223;
AC
XX
XX 14-OCT-2003 (first entry)
DT
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 102204.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
OS Homo sapiens.
XX

PN US2003104410-A1.
XX
XX 05-JUN-2003.
PD
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFRY-) AFRYMETRIX INC.
XX
PI Mitmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 102204; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 9 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 67.4%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 ACGGATCTCCTTCAC 19
DB 17 ACGTATCTCCTTCAC 2
RESULT 37
ACIO7104/C
ID ACIO7104 standard; DNA; 25 BP.
XX
XX ACIO7104;
AC
XX
XX 13-OCT-2003 (first entry)
DT
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 7095.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
OS Homo sapiens.
XX
XX US2003104410-A1.
PN

PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Miltmann MP;
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 7095; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense, match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridization to a DNA library,
 CC in analysis of genetic variation or in hybridization of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying allelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 11 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 67.4%; Score 12.8; DB 9; Length 25;
 Best Local Similarity 87.5%; Pred. No. 1e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 4 ACGGTATCTCCTTAC 19
 Db 17 ACGGTATCTACTTAC 2
 XX
 RESULT 38
 ACF79228
 ID ACF79228 standard; DNA; 25 BP.
 XX
 AC ACF79228;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human Nek2 reverse control oligonucleotide.
 XX
 KM Nek2; protein kinase; enzyme; human; cytosolic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003062197-A2.
 XX
 PD 31-JUL-2003.
 XX
 PF 24-JAN-2003; 2003WO-US002369.
 XX

PR 24-JAN-2002; 2002US-0352080P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Walter AO, Reinhard C;
 XX
 DR WPI; 2003-636724/60.
 XX
 XX
 FT New Nek2 inhibitor, useful for preparing a composition for treating
 FT neoplastic disease.
 XX
 PS Example 1; Page 55; 69pp; English.
 XX
 CC The present sequence is that of an oligonucleotide having the reverse
 CC sequence of CHIR-103-6 (see ACF79218), an antisense oligonucleotide
 CC targeted to human Nek2, a serine/threonine kinase involved in the
 CC regulation of mitosis. The oligonucleotide was used to transfect control
 CC cells in experiments designed to demonstrate the effect of antisense
 CC oligonucleotides on Nek2 mRNA levels in SW610 tumour cells. The antisense
 CC oligonucleotides inhibited Nek2 expression, inhibited cell proliferation
 CC and induced release of lactate dehydrogenase, indicating cell death. The
 CC invention provides Nek2 inhibitors, such as antisense oligonucleotides
 CC (see ACF79213-22) and ribozymes, that can be used to treat neoplastic
 CC disease (claimed). Methods are provided for modulating Nek2 expression
 CC and for regulating cell growth, particularly tumour cell growth
 XX
 SQ Sequence 25 BP; 4 A; 9 C; 4 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 67.4%; Score 12.8; DB 10; Length 25;
 Best Local Similarity 87.5%; Pred. No. 1e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 4 ACGGTATCTCCTTAC 19
 Db 5 ACGGTGCTCCTTAC 20
 XX
 RESULT 39
 AEA31091
 ID AEA31091 standard; DNA; 31 BP.
 XX
 AC AEA31091;
 XX
 DT 28-JUL-2005 (first entry)
 XX
 DE Hog cholera virus E2 antigen-related PCR primer 2.
 XX
 KM vaccine; livestock; vibrio cholerae infection; antibacterial;
 KM gastrointestinal disease; infection; antigen; PCR; primer; ss.
 XX
 OS Classical swine fever virus.
 XX
 OS Synthetic.
 XX
 PN CN1539989-A.
 XX
 PD 27-OCT-2004.
 XX
 PF 31-OCT-2003; 2003CN-01103408.
 XX
 PR 31-OCT-2003; 2003CN-01103408.
 XX
 PA (LANZ-) LANZHOU INST VETERINARY SURGEON CHINESE.
 XX
 PI Liu X, Han X, Xie Q;
 XX
 DR WPI; 2005-143329/16.
 XX
 PT Method for producing antigen protein in use for hog cholera vaccine.
 XX
 PS Claim 10; Page 3; 18pp; Chinese.
 XX
 CC The invention relates to a novel method for preparing an antigen protein
 CC to be used in a hog cholera vaccine. The method comprises extracting Hog

CC choleraeins RNA, reverse transcription to obtain the immune gene E2 of
CC Hog cholera virus, using E2 as template for PCR during insertion into an
CC expression carrier of Pichia yeast, introducing the recombinant
CC expression carrier to Pichia yeast, screening the recombinant Pichia
CC yeast, discriminating its expression product by testing its
CC immunoreactivity, determining the chosen recombinant yeast, testing and
CC analyzing its culture condition, choosing the optimal culture condition,
CC culturing the recombinant yeast and preparing the antigen protein of said
CC vaccine. The method of the invention may be useful for generating a hog
CC cholera vaccine. The current sequence is that of a Hog cholera virus E2
CC antigen-related PCR primer which was used in an exemplification of the
CC invention.

Query Match	67.4%	Score 12.8	DB 14	Length 31
Best Local Similarity	87.5%	Pred No. 1.1e+04		
Matches 14	Conservative 0	Mismatches 2	Indels 0	Gaps 0

Qy	4	ACGGTATCTCCTTAC	19
Db	9	ACGCTATCTCCTCAC	24

5Q Sequence 38 BP; 8 A; 9 C; 11 G; 10 T; 0 U; 0 Other;

Query Match	67.4%	Score 12.8	DB 11	Length 38
Best Local Similarity	87.5%	Pred. NO. 1.1e+04		
Matches 14	Conservative 0	Mismatches 2	Indels 0	Gaps 0

Qy	3	CACGGTATCTCCTTCA	11
Db	24	CACGATGTCCTCTCA	9

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 07:17:58 ; Search time 610 Seconds
(without alignments)
382.730 Million cell updates/sec

Title: US-10-636-065-29
Perfect score: 19
Sequence: 1 cgcacgcatctcttcac 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24308366

Minimum DB seq length: 0
Maximum DB seq length: 70

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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- 1: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US09_PUBCOMB.seq:*
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- 4: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	8	US-10-636-065-29
2	16.4	86.3	25	13	US-11-036-317-52322
3	16.4	86.3	25	13	US-11-036-317-753875
4	16	84.2	29	10	US-10-975-974-37
5	15.4	81.1	25	9	US-10-719-900-135048
6	15.4	81.1	25	11	US-10-934-048A-13794
7	15.4	81.1	25	11	US-10-934-048A-62245
8	14.8	77.9	25	10	US-10-956-157-190898
9	14.8	77.9	25	10	US-10-956-157-206582
10	14.8	77.9	25	10	US-10-956-157-219118
11	14.8	77.9	25	10	US-10-956-157-256107
12	14.8	77.9	25	10	US-10-956-157-274442
13	14.8	77.9	25	13	US-11-036-317-402065
14	14.8	77.9	25	13	US-11-036-317-753874
15	14.4	75.8	19	14	US-11-083-784-787223
16	14.4	75.8	19	15	US-11-101-244-787223
17	14.4	75.8	25	9	US-10-719-900-429169

C 18	14.4	75.8	25	10	US-10-956-157-235288	Sequence 235288,
C 19	14.4	75.8	25	13	US-11-060-756-282641	Sequence 282641,
C 20	14.4	75.8	25	13	US-11-060-756-282642	Sequence 282642,
C 21	14.2	74.7	22	11	US-10-310-914A-632065	Sequence 632065,
C 22	14.2	74.7	23	11	US-10-310-914A-632083	Sequence 632083,
C 23	14.2	74.7	25	13	US-11-036-317-811973	Sequence 811973,
C 24	14.2	74.7	19	7	US-10-400-382-29	Sequence 29, Appl
C 25	14	73.7	19	7	US-10-400-382-107	Sequence 107, Appl
C 26	14	73.7	19	10	US-10-975-790-107	Sequence 107, Appl
C 27	14	73.7	19	10	US-10-975-790-107	Sequence 107, Appl
C 28	14	73.7	25	8	US-10-681-773-6411	Sequence 6411, Ap
C 29	14	73.7	25	8	US-10-681-773-19055	Sequence 19055, A
C 30	14	73.7	25	8	US-10-681-773-29718	Sequence 29718, A
C 31	14	73.7	25	8	US-10-681-773-93340	Sequence 93340, A
C 32	14	73.7	25	8	US-10-681-773-95502	Sequence 95502, A
C 33	13.8	72.6	25	8	US-10-719-956-157200	Sequence 157200,
C 34	13.8	72.6	25	8	US-10-719-956-235231	Sequence 235231,
C 35	13.8	72.6	25	8	US-10-719-956-235231	Sequence 235231,
C 36	13.8	72.6	25	9	US-10-719-900-135047	Sequence 135047,
C 37	13.8	72.6	25	13	US-11-036-317-66927	Sequence 66927, A
C 38	13.8	72.6	25	13	US-11-036-317-488544	Sequence 488544,
C 39	13.8	72.6	25	13	US-11-036-317-531529	Sequence 531529,
C 40	13.8	72.6	25	13	US-11-036-317-691674	Sequence 691674,
C 41	13.8	72.6	25	13	US-11-036-317-691675	Sequence 691675,
C 42	13.8	72.6	25	13	US-11-036-317-778365	Sequence 778366,
C 43	13.8	72.6	25	13	US-11-036-317-826282	Sequence 826282,
C 44	13.8	72.6	25	15	US-11-121-849-406343	Sequence 406343,
C 45	13.8	72.6	25	15	US-11-121-849-419824	Sequence 419824,
C 46	13.8	72.6	25	16	US-11-136-527-236094	Sequence 236094,
C 47	13.8	72.6	59	2	US-08-781-986A-2496	Sequence 2496, Ap
C 48	13.8	72.6	59	8	US-10-329-624-2496	Sequence 2496, Ap
C 49	13.8	72.6	60	16	US-11-024-959-649	Sequence 649, App
C 50	13.4	70.5	19	14	US-11-083-784-798689	Sequence 798689,
C 51	13.4	70.5	19	15	US-11-101-244-798689	Sequence 798689,
C 52	13.4	70.5	25	13	US-11-060-756-212609	Sequence 212609,
C 53	13.4	70.5	25	13	US-11-060-756-212610	Sequence 212610,
C 54	13.4	70.5	25	13	US-11-121-849-530772	Sequence 530772,
C 55	13.4	70.5	25	16	US-11-136-527-290358	Sequence 290358,
C 56	13.4	70.5	50	16	US-11-175-859-20839	Sequence 20839, A
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C 61	13.2	69.5	25	8	US-10-719-956-139857	Sequence 139857,
C 62	13.2	69.5	25	10	US-10-956-157-198597	Sequence 198597,
C 63	13.2	69.5	25	10	US-10-956-157-198598	Sequence 198598,
C 64	13.2	69.5	25	10	US-10-956-157-293738	Sequence 293739,
C 65	13.2	69.5	25	11	US-10-956-157-293739	Sequence 293739,
C 66	13.2	69.5	25	11	US-10-933-982-123966	Sequence 123966,
C 67	13.2	69.5	25	11	US-10-933-982-164554	Sequence 164554,
C 68	13.2	69.5	25	11	US-10-934-084A-26745	Sequence 26745, A
C 69	13.2	69.5	25	13	US-11-036-317-483348	Sequence 483348,
C 70	13.2	69.5	25	13	US-11-121-849-356633	Sequence 356633,
C 71	13.2	69.5	25	16	US-11-136-527-61220	Sequence 61220, A
C 72	13.2	69.5	25	16	US-11-136-527-61225	Sequence 61225, A
C 73	13.2	69.5	25	16	US-11-136-527-61240	Sequence 61240, A
C 74	13.2	69.5	25	16	US-11-136-527-61242	Sequence 61242, A
C 75	13.2	69.5	25	16	US-11-136-527-61251	Sequence 61251, A
C 76	13.2	69.5	42	7	US-10-396-488-4	Sequence 4, Appl1
C 77	13.2	69.5	65	3	US-09-908-975-931	Sequence 931, App
C 78	13.2	69.5	19	10	US-10-739-904-10	Sequence 10, Appl
C 79	13	68.4	19	14	US-11-083-784-1156068	Sequence 1156068,
C 80	13	68.4	19	15	US-11-101-244-1156068	Sequence 1156068,
C 81	13	68.4	25	9	US-10-719-900-188836	Sequence 188836,
C 82	13	68.4	25	9	US-10-719-900-87646	Sequence 87646,
C 83	13	68.4	25	13	US-11-036-317-842026	Sequence 842026,
C 84	13	68.4	25	13	US-11-036-317-842221	Sequence 842221,
C 85	13	68.4	19	14	US-11-083-784-224158	Sequence 224158,
C 86	12.8	67.4	19	14	US-11-083-784-761475	Sequence 761475,
C 87	12.8	67.4	19	15	US-11-101-244-224158	Sequence 224158,
C 88	12.8	67.4	19	15	US-11-101-244-761475	Sequence 761475,
C 89	12.8	67.4	20	11	US-10-310-914A-973196	Sequence 973196,
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91 12.8 67.4 21 9 US-10-751-736-15045 Sequence 15045, A
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94 12.8 67.4 21 10 US-10-770-726-27622 Sequence 27622, A
95 12.8 67.4 21 10 US-10-770-726-28015 Sequence 28015, A
96 12.8 67.4 21 10 US-10-770-726-28102 Sequence 28102, A
97 12.8 67.4 22 11 US-10-809-945-27 Sequence 27, Appl
98 12.8 67.4 22 11 US-10-809-945-29 Sequence 29, Appl
99 12.8 67.4 23 10 US-10-809-945-29 Sequence 29, Appl
c 100 12.8 67.4 23 11 US-10-310-914A-1379474 Sequence 1379474,
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ALIGNMENTS

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RESULT 1
US-10-636-065-29
; Sequence 29, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens
US-10-636-065-29
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Query Match          100.0%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGCAGGTATCTCTTCAC 19
DB 1 CGCAGGTATCTCTTCAC 19
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RESULT 2

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US-11-036-317-52322/C
; Sequence 52322, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 52322
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-52322
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Query Match          86.3%; Score 16.4; DB 13; Length 25;
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Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 25 GCACGGTATCTCTTCAC 8
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RESULT 3

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US-11-036-317-753875/C
; Sequence 753875, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 753875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-753875
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Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2 GCACGGTATCTCTTCAC 19
DB 25 GCACGGTATCTCTTCAC 8
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RESULT 4

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US-10-975-974-37/C
; Sequence 37, Application US/10975974
; Publication No. US20050148535A1
; GENERAL INFORMATION:
; APPLICANT: Lacasse, Eric
; APPLICANT: McManus, Daniel
; TITLE OF INVENTION: IAP NUCLEOBASE OLIGOMERS AND OLIGOMERIC
; TITLE OF INVENTION: COMPLEXES AND USES THEREOF
; FILE REFERENCE: 07891/038002
; CURRENT APPLICATION NUMBER: US/10/975,974
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: 60/516,192
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2, 5, 8, 17, 22, 27
; OTHER INFORMATION: n = T or U
; OTHER INFORMATION: based on Homo sapiens
; OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,
; OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog
US-10-975-974-37
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Query Match          84.2%; Score 16; DB 10; Length 29;
Best Local Similarity 84.2%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 GCACGGTATCTCTTCAC 19
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Db 25 GCACGGGTATCTCCTTCA 7

RESULT 5

US-10-719-900-135048
; Sequence 135048, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 135048
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-135048

Query Match 81.1%; Score 15.4; DB 9; Length 25;
Best Local Similarity 94.1%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACGGGTATCTCCTTCA 18
| | | | | | | | | | | | | | | | | | | | |
Db 8 GCACGGGTATCTCCTTCA 24

RESULT 6

US-10-934-048A-13794
; Sequence 13794, Application US/10934048A
; Publication No. US20060051770A1
; GENERAL INFORMATION:
; APPLICANT: Tanya Makeev
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3699
; CURRENT APPLICATION NUMBER: US/10/934,048A
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 120855
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13794
; LENGTH: 25
; TYPE: DNA
; ORGANISM: S. cerevisiae
US-10-934-048A-13794

Query Match 81.1%; Score 15.4; DB 11; Length 25;
Best Local Similarity 94.1%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACGGGTATCTCCTTCA 18
| | | | | | | | | | | | | | | | | | | | |
Db 8 GCACGGGTATCTCCTTCA 24

RESULT 7

US-10-934-048A-62245
; Sequence 62245, Application US/10934048A
; Publication No. US20060051770A1
; GENERAL INFORMATION:
; APPLICANT: Tanya Makeev
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3699
; CURRENT APPLICATION NUMBER: US/10/934,048A
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 120855
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 62245

LENGTH: 25
; TYPE: DNA
; ORGANISM: S. cerevisiae
US-10-934-048A-62245

Query Match 81.1%; Score 15.4; DB 11; Length 25;
Best Local Similarity 94.1%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACGGGTATCTCCTTCA 18
| | | | | | | | | | | | | | | | | | | | |
Db 3 GCACGGGTATCTCCTTCA 19

RESULT 8

US-10-956-157-190898/c
; Sequence 190898, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 190898
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-190898

Query Match 77.9%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGGTATCTCCTTCA 19
| | | | | | | | | | | | | | | | | | | | |
Db 22 GAACGGGTATCTCCTTCA 5

RESULT 9

US-10-956-157-206582/c
; Sequence 206582, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206582
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-206582

Query Match 77.9%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGGTATCTCCTTCA 19
| | | | | | | | | | | | | | | | | | | | |
Db 23 GAACGGGTATCTCCTTCA 6

RESULT 10

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US-10-956-157-219118/c
; Sequence 219118, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 2004-10-04
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 219118
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-219118

Query Match      77.9%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCACGGTATCTCCTTCAC 19
Db      21 GAACGGTGTCTCCTTCAC 4

RESULT 11
US-10-956-157-256107/c
; Sequence 256107, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 2004-10-04
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 256107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-256107

Query Match      77.9%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCACGGTATCTCCTTCAC 19
Db      25 GAACGGTGTCTCCTTCAC 8

RESULT 12
US-10-956-157-274442/c
; Sequence 274442, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 2004-10-04
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274442
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-274442

Query Match      77.9%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCACGGTATCTCCTTCAC 19
Db      24 GAACGGTGTCTCCTTCAC 7

RESULT 13
US-11-036-317-402065
; Sequence 402065, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 402065
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-402065

Query Match      77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCACGGTATCTCCTTCAC 19
Db      4 GCACGGTATCTCCTTCAC 21

RESULT 14
US-11-036-317-753874/c
; Sequence 753874, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 753874
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-753874

Query Match      77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCACGGTATCTCCTTCAC 19
Db      25 GCACGGTGTCTCCTTCAC 8
```


RESULT 15

US-11-083-784-787223/C
 ; Sequence 787223, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 134990US
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR FILING DATE: 2005-03-18
 ; PRIOR APPLICATION NUMBER: US/10/714,333
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 787223
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-787223

Query Match 75.8%; Score 14.4; DB 14; Length 19;
 Best Local Similarity 93.8%; Pred. No. 2.4e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGATCTCCTTCA 18
 |||||
 DB 16 CACGGATCTCCTTCA 1

RESULT 16

US-11-101-244-787223/C
 ; Sequence 787223, Application US/1101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 134990US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 787223
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-787223

Query Match 75.8%; Score 14.4; DB 15; Length 19;
 Best Local Similarity 93.8%; Pred. No. 2.4e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGATCTCCTTCA 18
 |||||
 DB 16 CACGGATCTCCTTCA 1

RESULT 17

US-10-719-900-429169/C
 ; Sequence 429169, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Method of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 429169
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-429169

Query Match 75.8%; Score 14.4; DB 9; Length 25;
 Best Local Similarity 93.8%; Pred. No. 2.5e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACGGATCTCCTTC 17
 |||||
 DB 16 GCACGGATCTCCTTC 1

RESULT 18

US-10-956-157-235288/C
 ; Sequence 235288, Application US/10956157
 ; Publication No. US20050118625A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
 ; FILE REFERENCE: 031896-043000 (AM 101081)
 ; CURRENT APPLICATION NUMBER: US/10/956,157
 ; CURRENT FILING DATE: 2004-10-04
 ; NUMBER OF SEQ ID NOS: 319805
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 235288
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Probe Sequence
 US-10-956-157-235288

Query Match 75.8%; Score 14.4; DB 10; Length 25;
 Best Local Similarity 93.8%; Pred. No. 2.5e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ACGGTATCTCCTTCA 19
 |||||
 DB 25 ACGGTATCTCCTTCA 10

RESULT 19

US-11-060-756-282641/C
 ; Sequence 282641, Application US/11060756
 ; Publication No. US20050221354A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William Martin
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
 ; FILE REFERENCE: AM101083 (031896-042000)
 ; CURRENT APPLICATION NUMBER: US/11/060,756
 ; CURRENT FILING DATE: 2005-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2

```
; SEQ ID NO 282641
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-282641
```

```
Query Match          75.8%; Score 14.4; DB 13; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ACGGATCTCTCTTCAC 19
         |||||
Db      25 ACGGAATCTCTTCAC 10
```

```
RESULT 20
US-11-060-756-282642/C
; Sequence 282642, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 282642
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-282642
```

```
Query Match          75.8%; Score 14.4; DB 13; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ACGGATCTCTCTTCAC 19
         |||||
Db      25 ACGGAATCTCTTCAC 10
```

```
RESULT 21
US-10-310-914A-632065
; Sequence 632065, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 632065
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-632065
```

```
Query Match          74.7%; Score 14.2; DB 11; Length 22;
Best Local Similarity 73.7%; Pred. No. 3.1e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CGCAGGATCTCTCTTCAC 19
         |||||
Db      2 CGCAGCGAUCUCCCGCAC 20
```

```
RESULT 22
US-10-310-914A-632083
; Sequence 632083, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 632083
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-632083
```

```
Query Match          74.7%; Score 14.2; DB 11; Length 23;
Best Local Similarity 73.7%; Pred. No. 3.1e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CGCAGGATCTCTCTTCAC 19
         |||||
Db      4 CGCAGCGAUCUCCCGCAC 22
```

```
RESULT 23
US-11-036-317-811973
; Sequence 811973, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 811973
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-811973
```

```
Query Match          74.7%; Score 14.2; DB 13; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CGCAGGATCTCTCTTCAC 19
         |||||
Db      6 CACACGGTCTCTACTTCAC 24
```

```
RESULT 24
US-10-400-382-29
; Sequence 29, Application US/10400382
; Publication No. US20030190659A1
; GENERAL INFORMATION:
; APPLICANT: Lacasse, Eric
; APPLICANT: McManus, Daniel
; APPLICANT: Durkin, Jonathan P.
; TITLE OF INVENTION: Antisense iAP Nucleobase Oligomers and
; FILE REFERENCE: 07891/025004
; CURRENT APPLICATION NUMBER: US/10/400,382
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/367,853
```

PRIOR FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: based on Homo sapiens.
OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,
OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog
FEATURE:
NAME/KEY: misc feature
LOCATION: 8, 10, 12, 15, 16
OTHER INFORMATION: n = T or U
US-10-400-382-29

Query Match 73.7%; Score 14; DB 7; Length 19;
Best Local Similarity 73.7%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCCTTCAC 19
Db 1 CGCAGCGNANNCNNCNCAC 19

RESULT 25
US-10-400-382-107
Sequence 107, Application US/10400382
Publication No. US20030190659A1
GENERAL INFORMATION:
APPLICANT: Lacasse, Eric
APPLICANT: McManus, Daniel
APPLICANT: Durkin, Jonathan P.
TITLE OF INVENTION: Antisense IAP Nucleobase Oligomers and
FILE REFERENCE: 07891/025004
CURRENT APPLICATION NUMBER: US/10/400,382
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/367,853
PRIOR FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 107

LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: based on Homo sapiens.
OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,
OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog
FEATURE:
NAME/KEY: misc feature
LOCATION: 8, 10, 12, 15, 16
OTHER INFORMATION: n = T or U
US-10-400-382-107

Query Match 73.7%; Score 14; DB 7; Length 19;
Best Local Similarity 73.7%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCCTTCAC 19
Db 1 CGCAGCGNANNCNNCNCAC 19

RESULT 26
US-10-975-790-29
Sequence 29, Application US/10975790
Publication No. US20050119217A1
GENERAL INFORMATION:
APPLICANT: Lacasse, Eric
APPLICANT: McManus, Daniel

APPLICANT: Durkin, Jonathan, P.
TITLE OF INVENTION: METHODS AND REAGENTS FOR THE TREATMENT
OF PROLIFERATIVE DISEASES
FILE REFERENCE: 07891/039002
CURRENT APPLICATION NUMBER: US/10/975,790
CURRENT FILING DATE: 2004-10-28
PRIOR APPLICATION NUMBER: 60/516,263
PRIOR FILING DATE: 2003-10-30
NUMBER OF SEQ ID NOS: 490
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: based on Homo sapiens.
OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,
OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog
FEATURE:
NAME/KEY: misc feature
LOCATION: 8, 10, 12, 15, 16
OTHER INFORMATION: n = T or U
US-10-975-790-29

Query Match 73.7%; Score 14; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCCTTCAC 19
Db 1 CGCAGCGNANNCNNCNCAC 19

RESULT 27
US-10-975-790-107
Sequence 107, Application US/10975790
Publication No. US20050119217A1
GENERAL INFORMATION:
APPLICANT: Lacasse, Eric
APPLICANT: McManus, Daniel
APPLICANT: Durkin, Jonathan, P.
TITLE OF INVENTION: METHODS AND REAGENTS FOR THE TREATMENT
OF PROLIFERATIVE DISEASES
FILE REFERENCE: 07891/039002
CURRENT APPLICATION NUMBER: US/10/975,790
CURRENT FILING DATE: 2004-10-28
PRIOR APPLICATION NUMBER: 60/516,263
PRIOR FILING DATE: 2003-10-30
NUMBER OF SEQ ID NOS: 490
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 107
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: based on Homo sapiens.
OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,
OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog
FEATURE:
NAME/KEY: misc feature
LOCATION: 8, 10, 12, 15, 16
OTHER INFORMATION: n = T or U
US-10-975-790-107

Query Match 73.7%; Score 14; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCCTTCAC 19
Db 1 CGCAGCGNANNCNNCNCAC 19

```
RESULT 28
US-10-681-773-6411/c
; Sequence 6411, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Mei, Rui
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 6411
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-6411
```

```
Query Match      73.7%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
Db      16 ACGGTATCTCCTTC 3
```

```
RESULT 29
US-10-681-773-19055/c
; Sequence 19055, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 19055
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-19055
```

```
Query Match      73.7%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
Db      15 ACGGTATCTCCTTC 2
```

```
RESULT 30
US-10-681-773-29718/c
; Sequence 29718, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 29718
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-29718
```

```
Query Match      73.7%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
Db      19 ACGGTATCTCCTTC 6
```

```
RESULT 31
US-10-681-773-93340/c
; Sequence 93340, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 93340
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-93340
```

```
Query Match      73.7%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
Db      20 ACGGTATCTCCTTC 7
```

```
RESULT 32
US-10-681-773-95502/c
; Sequence 95502, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
```

```
FILE REFERENCE: 3522.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/417,190
PRIOR FILING DATE: 2002-10-08
NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 95502
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-681-773-95502
```

```
Query Match      73.7%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 4 ACAGTATCTCTTC 17
| | | | | | | | | |
Db 18 ACAGTATCTCTTC 5

```
RESULT 33
US-10-719-956-157200
Sequence 157200, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 157200
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-157200
```

```
Query Match      72.6%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 3 CACGATCTCTCTC 19
| | | | | | | | | |
Db 4 CACGATCTCTCTC 20

```
RESULT 34
US-10-719-956-235231/c
Sequence 235231, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 235231
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-235231
```

```
Query Match      72.6%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 3 CACGATCTCTCTC 19
| | | | | | | | | |
Db 19 CTCGATCTCTCTC 3

```
RESULT 35
US-10-719-956-317851/c
Sequence 317851, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 317851
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-317851
```

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Query Match      72.6%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 GCAGGATCTCTCTCA 18
| | | | | | | | | |
Db 24 GCAGGATCTCTCTCA 8

```
RESULT 36
US-10-719-900-135047
Sequence 135047, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 135047
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-135047
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Query Match      72.6%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 GCAGGATCTCTCTCA 18
| | | | | | | | | |
Db 8 GCAGGATCTCTCTCA 24

```
RESULT 37
US-11-036-317-66927/c
Sequence 66927, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
```

```

; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; NUMBER OF SEQ ID NOS: 60/536,639
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 66927
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-66927
```

```

Query Match      72.6%; Score 13.8; DB 13; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      2 GCACGGATCTCTCTTCA 18
Db      21 GCACGGATCTCTTCTTCA 5
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RESULT 38
US-11-036-317-488544/c
; Sequence 488544, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; NUMBER OF SEQ ID NOS: 60/536,639
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 488544
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-488544
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```

Query Match      72.6%; Score 13.8; DB 13; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      2 GCACGGATCTCTCTTCA 18
Db      21 GCACGGATCTCTTCTTCA 5
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```

RESULT 39
US-11-036-317-531529/c
; Sequence 531529, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; NUMBER OF SEQ ID NOS: 60/536,639
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 531529
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
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```
US-11-036-317-531529
```

```

Query Match      72.6%; Score 13.8; DB 13; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 GCACGGATCTCTCTTCA 18
Db      20 GTACGGATCTCTTCTTCA 4
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```

RESULT 40
US-11-036-317-691674/c
; Sequence 691674, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; NUMBER OF SEQ ID NOS: 60/536,639
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 691674
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-691674
```

```

Query Match      72.6%; Score 13.8; DB 13; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      2 GCACGGATCTCTCTTCA 18
Db      19 GTACGGATCTCTTCTTCA 3
```

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Search completed: August 10, 2006, 08:37:29
Job time : 613 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model1

Run on: August 10, 2006, 08:07:12 ; Search time 87.6667 Seconds
(without alignments)
344.184 Million cell updates/sec

Title: US-10-636-065-29
Perfect score: 19
Sequence: 1 cgcacgcgtactctcttcac 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 3071694

Minimum DB seq length: 0
Maximum DB seq length: 70

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

- 1: /EMC_Ceiera_SIDS3/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Ceiera_SIDS3/prodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Ceiera_SIDS3/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Ceiera_SIDS3/prodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Ceiera_SIDS3/prodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Ceiera_SIDS3/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Ceiera_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Ceiera_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 9: /EMC_Ceiera_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 10: /EMC_Ceiera_SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.4	70.5	25	US-11-348-413-698648	Sequence 698648,
2	13.4	70.5	25	US-11-348-413-698649	Sequence 698649,
3	13.4	70.5	25	US-11-348-413-698650	Sequence 698650,
4	13.2	69.5	25	US-11-217-529-106544	Sequence 106544,
5	13.2	69.5	25	US-11-348-413-45911	Sequence 45911, A
6	13.2	69.5	25	US-11-348-413-45912	Sequence 45912, A
7	13.2	69.5	25	US-11-348-413-63497	Sequence 63497, A
8	13.2	69.5	25	US-11-281-495-4	Sequence 4954,
9	13.2	69.5	25	US-11-348-413-684532	Sequence 684532,
10	12.8	67.4	25	US-11-217-529-164386	Sequence 164386,
11	12.8	67.4	25	US-11-348-413-251718	Sequence 251718,
12	12.8	67.4	25	US-11-348-413-251719	Sequence 251719,
13	12.8	67.4	25	US-11-348-413-865498	Sequence 865498,
14	12.8	67.4	25	US-11-297-810-26	Sequence 26, Appl
15	12.8	67.4	25	US-11-314-941-26	Sequence 26, Appl
16	12.6	66.3	25	US-11-217-529-141152	Sequence 141152,
17	12.6	66.3	25	US-11-348-413-198939	Sequence 198939,
18	12.6	66.3	25	US-11-348-413-810033	Sequence 810033,
19	12.6	66.3	50	US-10-511-937-136	Sequence 136, App
20	12.6	66.3	50	US-10-554-711-392	Sequence 392, App
21	12.4	65.3	25	US-11-348-413-257483	Sequence 257483,
22	12.4	65.3	25	US-11-348-413-257484	Sequence 257484,
23	12.4	65.3	25	US-11-348-413-257485	Sequence 257485,

C 24	12.4	65.3	25	US-11-348-413-257486	Sequence 257486,
C 25	12.4	65.3	25	US-11-348-413-857440	Sequence 857440,
C 26	12.4	65.3	25	US-11-348-413-871598	Sequence 871598,
C 27	12.4	65.3	25	US-11-348-413-871599	Sequence 871599,
C 28	12.4	65.3	31	US-11-240-651-32	Sequence 32, Appl
C 29	12.4	65.3	60	US-11-240-651-14	Sequence 14, Appl
C 30	12.2	64.2	25	US-11-348-413-429142	Sequence 429142,
C 31	12.2	64.2	25	US-11-348-413-636110	Sequence 636110,
C 32	12.2	64.2	25	US-11-348-413-661408	Sequence 661408,
C 33	12.2	64.2	25	US-11-348-413-661409	Sequence 661409,
C 34	12.2	64.2	25	US-11-348-413-701530	Sequence 701530,
C 35	12.2	64.2	25	US-11-348-413-812478	Sequence 812478,
C 36	12.2	63.2	25	US-11-348-413-90099	Sequence 90099, A
C 37	12.2	63.2	25	US-11-348-413-90100	Sequence 90100, A
C 38	12.2	63.2	25	US-11-348-413-90101	Sequence 90101, A
C 39	12.2	63.2	25	US-11-348-413-208705	Sequence 208705,
C 40	12.2	63.2	25	US-11-348-413-208706	Sequence 208706,
C 41	12.2	63.2	25	US-11-348-413-208707	Sequence 208707,
C 42	12.2	63.2	25	US-11-348-413-208708	Sequence 208708,
C 43	12.2	63.2	25	US-11-348-413-208709	Sequence 208709,
C 44	12.2	63.2	25	US-11-348-413-443433	Sequence 443433,
C 45	12.2	63.2	25	US-11-348-413-443434	Sequence 443434,
C 46	12.2	63.2	25	US-11-348-413-443435	Sequence 443435,
C 47	12.2	63.2	25	US-11-348-413-597319	Sequence 597319,
C 48	12.2	63.2	25	US-11-348-413-597320	Sequence 597320,
C 49	12.2	63.2	25	US-11-348-413-597321	Sequence 597321,
C 50	12.2	63.2	25	US-11-348-413-597322	Sequence 597322,
C 51	12.2	63.2	25	US-11-348-413-597818	Sequence 597818,
C 52	12.2	63.2	25	US-11-348-413-597819	Sequence 597819,
C 53	12.2	63.2	25	US-11-348-413-597820	Sequence 597820,
C 54	12.2	63.2	25	US-11-348-413-597821	Sequence 597821,
C 55	12.2	63.2	25	US-11-348-413-634498	Sequence 634498,
C 56	12.2	63.2	25	US-11-348-413-681024	Sequence 681024,
C 57	12.2	63.2	25	US-11-348-413-793930	Sequence 793930,
C 58	12.2	63.2	25	US-11-348-413-793931	Sequence 793931,
C 59	12.2	63.2	25	US-11-348-413-820166	Sequence 820166,
C 60	12.2	63.2	25	US-11-348-413-820167	Sequence 820167,
C 61	12.2	63.2	25	US-11-348-413-1085116	Sequence 1085116,
C 62	12.2	63.2	25	US-11-348-413-1267794	Sequence 1267794,
C 63	12.2	63.2	25	US-11-348-413-1267795	Sequence 1267795,
C 64	12.2	63.2	25	US-11-348-413-1267796	Sequence 1267796,
C 65	12.2	63.2	25	US-11-348-413-1268372	Sequence 1268372,
C 66	12.2	63.2	25	US-11-348-413-1268373	Sequence 1268373,
C 67	12.2	63.2	25	US-11-348-413-1268374	Sequence 1268374,
C 68	12.2	63.2	25	US-11-348-413-1268375	Sequence 1268375,
C 69	12.2	63.2	25	US-11-348-413-1268376	Sequence 1268376,
C 70	12.2	63.2	25	US-11-348-413-1268377	Sequence 1268377,
C 71	11.8	62.1	25	US-11-217-529-45056	Sequence 45056, A
C 72	11.8	62.1	25	US-11-217-529-141477	Sequence 141477,
C 73	11.8	62.1	25	US-11-217-529-145207	Sequence 145207,
C 74	11.8	62.1	25	US-11-217-529-147920	Sequence 147920,
C 75	11.8	62.1	25	US-11-217-529-160598	Sequence 160598,
C 76	11.8	62.1	25	US-11-217-529-186459	Sequence 186459,
C 77	11.8	62.1	25	US-11-348-413-101807	Sequence 101807,
C 78	11.8	62.1	25	US-11-348-413-238982	Sequence 238982,
C 79	11.8	62.1	25	US-11-348-413-238983	Sequence 238983,
C 80	11.8	62.1	25	US-11-348-413-238984	Sequence 238984,
C 81	11.8	62.1	25	US-11-348-413-251717	Sequence 251717,
C 82	11.8	62.1	25	US-11-348-413-445915	Sequence 445915,
C 83	11.8	62.1	25	US-11-348-413-445916	Sequence 445916,
C 84	11.8	62.1	25	US-11-348-413-445917	Sequence 445917,
C 85	11.8	62.1	25	US-11-348-413-445918	Sequence 445918,
C 86	11.8	62.1	25	US-11-348-413-445919	Sequence 445919,
C 87	11.8	62.1	25	US-11-348-413-445920	Sequence 445920,
C 88	11.8	62.1	25	US-11-348-413-613537	Sequence 613537,
C 89	11.8	62.1	25	US-11-348-413-613538	Sequence 613538,
C 90	11.8	62.1	25	US-11-348-413-636337	Sequence 636337,
C 91	11.8	62.1	25	US-11-348-413-693357	Sequence 693357,
C 92	11.8	62.1	25	US-11-348-413-791363	Sequence 791363,
C 93	11.8	62.1	25	US-11-348-413-794460	Sequence 794460,
C 94	11.8	62.1	25	US-11-348-413-831294	Sequence 831294,
C 95	11.8	62.1	25	US-11-348-413-851672	Sequence 851672,
C 96	11.8	62.1	25	US-11-348-413-851673	Sequence 851673,

	C 97	11.8	62.1	25	9	US-11-348-413-851674
	C 98	11.8	62.1	25	9	US-11-348-413-877430
	C 99	11.8	62.1	25	9	US-11-348-413-1035845
	C 100	11.8	62.1	25	9	US-11-348-413-1091924

	Sequence 851674,
	Sequence 877430,
	Sequence 1035845,
	Sequence 1091924,

ALIGNMENTS

RESULT 1

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US-11-348-413-698648/c
; Sequence 698648, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 698648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2598; WANO1UNSL_at; Start 163; Stop 187;
; OTHER INFORMATION: 11111100000000
US-11-348-413-698648

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Query Match Best Local Similarity 70.5%; Score 13.4; DB 9; Length 25;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACGTAATCTCCTT 16
 Db 25 GCACGTAATCTCCTT 11

RESULT 2

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US-11-348-413-698649/c
; Sequence 698649, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 698649
; LENGTH: 25

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	TYPE: DNA
	ORGANISM: Artificial
	FEATURE:
	OTHER INFORMATION: probe
	FEATURE:
	NAME/KEY: misc.feature
	LOCATION: (1)..(25)
	OTHER INFORMATION: SEQ ID NO: 2598; WANO1UNSL_at; Start 164; Stop 188;
	OTHER INFORMATION: 11111100000000

US-11-348-413-698649

Query Match Best Local Similarity 70.5%; Score 13.4; DB 9; Length 25;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACGTAATCTCCTT 16
 Db 24 GCACGTAATCTCCTT 10

RESULT 3

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US-11-348-413-698650/c
; Sequence 698650, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 698650
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2598; WANO1UNSL_at; Start 167; Stop 191;
; OTHER INFORMATION: 11111100000000
US-11-348-413-698650

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Query Match Best Local Similarity 70.5%; Score 13.4; DB 9; Length 25;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACGTAATCTCCTT 16
 Db 21 GCACGTAATCTCCTT 7

RESULT 4

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US-11-217-529-106544/c
; Sequence 106544, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

```


TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 106544
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-106544

Query Match 69.5%; Score 13.2; DB 8; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTCA 18
Db 25 CTCAGGTAACTCCTTCA 8

RESULT 5
US-11-348-413-45911/c
Sequence 45911, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 45911
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
NAME/KEY: misc feature
LOCATION: (1)-(25)
OTHER INFORMATION: SEQ ID NO: 779; WAN01UJNW; Start 469; Stop 493;
US-11-348-413-45911

Query Match 69.5%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTCA 18
Db 20 CGCAGGTATCTAAATCA 3

RESULT 6
US-11-348-413-45912/c
Sequence 45912, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen

APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 45912
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
NAME/KEY: misc feature
LOCATION: (1)-(25)
OTHER INFORMATION: SEQ ID NO: 779; WAN01UJNW; Start 470; Stop 494;
US-11-348-413-45912

Query Match 69.5%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTCA 18
Db 19 CGCAGGTATCTAAATCA 2

RESULT 7
US-11-348-413-634497/c
Sequence 634497, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 634497
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
NAME/KEY: misc feature
LOCATION: (1)-(25)
OTHER INFORMATION: SEQ ID NO: 779; WAN01UJNW; Start 467; Stop 491;
US-11-348-413-634497

Query Match 69.5%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTCA 18

Db 22 CGCAGCATCTAATCA 5

RESULT 8

US-11-281-495-4
; Sequence 4, Application US/11281495
; Publication No. US20060115878A1
; GENERAL INFORMATION:
; APPLICANT: HARA, YOSHIHIKO
; APPLICANT: IZUI, HIROSHI
; APPLICANT: ASANO, TAKAHITO
; APPLICANT: WATANABE, YASUYUKI
; APPLICANT: NAKAMATSU, TSUYOSHI
; TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACID
; FILE REFERENCE: 235806US0
; CURRENT APPLICATION NUMBER: US/11/281,495
; PRIOR FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: US/10/396,488
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: JP 2002-088668
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-281-495-4

Query Match

69.5%; Score 13.2; DB 8; Length 42;
Best Local Similarity 83.3%; Pred. No. 8.e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGCATCTCTCTCA 18
||| ||| ||| ||| |||
Db 2 CGCAGCATCTCTCTCA 19

RESULT 9

US-11-348-413-684532/C
; Sequence 684532, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Murthy, William M
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 684532
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2204; WANOIUXA_at; Start 652; Stop 676;
US-11-348-413-684532

Query Match 68.4%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CACGATCTCTCT 15
||| ||| ||| ||| |||
Db 18 CACGATCTCTCT 6

RESULT 10

US-11-217-529-164386
; Sequence 164386, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 164386
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-164386

Query Match 67.4%; Score 12.8; DB 8; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGATCTCTCTC 17
||| ||| ||| ||| |||
Db 4 GCACGATCTCTCTC 19

RESULT 11

US-11-348-413-251718
; Sequence 251718, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Murthy, William M
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 251718
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7331; WANOIUMEN; Start 11; Stop 35;
US-11-348-413-251718

OTHER INFORMATION: 00000001100000
US-11-348-413-251718

Query Match 67.4%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 CACGATCTCTCTCA 18
DB 10 CACGATCTCTCTCA 25

RESULT 12

US-11-348-413-251719
Sequence 251719, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT FILING DATE: 2006-02-07
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 251719
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
NAME/KEY: misc_feature
LOCATION: (1..(25))
OTHER INFORMATION: SEQ ID NO: 7331; WANO1UM6N; Start 12; Stop 36;
OTHER INFORMATION: 00000001100000
US-11-348-413-251719

Query Match 67.4%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 CACGATCTCTCTCA 18
DB 9 CACGATCTCTCTCA 24

RESULT 13

US-11-348-413-865498
Sequence 865498, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT FILING DATE: 2006-02-07
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05

NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 865498
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe

NAME/KEY: misc_feature
LOCATION: (1..(25))
OTHER INFORMATION: SEQ ID NO: 7331; WANO1UM6N_at; Start 12; Stop 36;
OTHER INFORMATION: 00000001100000
US-11-348-413-865498

Query Match 67.4%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 CACGATCTCTCTCA 18
DB 9 CACGATCTCTCTCA 24

RESULT 14

US-11-297-810-26/C
Sequence 26, Application US/11297810
Publication No. US2006012037A1
GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter
APPLICANT: Chirayeb, John
APPLICANT: Knight, David
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of Human
FILE REFERENCE: 0975,1005-049
CURRENT APPLICATION NUMBER: US/11/297,810
CURRENT FILING DATE: 2005-12-08
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: U.S. 09/927,703
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: U.S. 09/756,398
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: U.S. 09/133,119
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: U.S. 08/570,674
PRIOR FILING DATE: 1995-12-11
PRIOR APPLICATION NUMBER: U.S. 08/324,799
PRIOR FILING DATE: 1994-10-18
PRIOR APPLICATION NUMBER: U.S. 08/192,102
PRIOR FILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,861
PRIOR FILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR FILING DATE: 1993-01-29
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR FILING DATE: 1993-02-02
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 52
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Partial sequence of pLC871
US-11-297-810-26

Query Match 67.4%; Score 12.8; DB 8; Length 52;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGGTATCTCCTTCA 18
| | | | | | | | | |
Db 27 CCGGATATCTCCTTCA 12

RESULT 15

US-11-314-941-26/c
; Sequence 26, Application US/11314941
; Publication No. US20060140949A1
; GENERAL INFORMATION:
; APPLICANT: Ie, Junning
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Human Anti-TNF Antibodies and Peptides
; FILE REFERENCE: 0975.1005-059
; CURRENT APPLICATION NUMBER: US/11/314, 941
; PRIOR FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: U.S. 10/198,845
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 26
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial sequence of pLC871
; US-11-314-941-26

Query Match 67.4%; Score 12.8; DB 9; Length 52;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGGTATCTCCTTCA 18
| | | | | | | | | |
Db 27 CCGGATATCTCCTTCA 12

RESULT 16

US-11-217-529-141152
; Sequence 14152, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SONTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOMO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 141152
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-141152

Query Match 66.3%; Score 12.6; DB 8; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCGACGGTATCTCCTTAC 19
| | | | | | | | | |
Db 3 CGTACGTATTTCTTCTAC 21

RESULT 17
US-11-348-413-198939/c
; Sequence 198939, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 198939
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc.feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 5880; WAN01UJ5C; Start 707; Stop 731;
; US-11-348-413-198939

Query Match 66.3%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCGACGGTATCTCCTTAC 19
| | | | | | | | | |
Db 19 CGCTCGTATCTCTCTTAC 1

RESULT 18
US-11-348-413-810033/c
; Sequence 810033, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen

;; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
;; FILE REFERENCE: 031896-084100 (AM 101724)
;; CURRENT APPLICATION NUMBER: US/11/348,413
;; CURRENT FILING DATE: 2006-02-07
;; PRIOR APPLICATION NUMBER: PCT/US05/035471
;; PRIOR FILING DATE: 2005-10-05
;; PRIOR APPLICATION NUMBER: US 11/243,445
;; PRIOR FILING DATE: 2005-10-05
;; PRIOR APPLICATION NUMBER: US 60/615,573
;; PRIOR FILING DATE: 2004-10-05
;; NUMBER OF SEQ ID NOS: 1276209
;; SEQ ID NO 810033
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: probe
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(25)
;; OTHER INFORMATION: SEQ ID NO: 5880; WAN01U5C_at; Start 701; Stop 725;
;; OTHER INFORMATION: 000000011100000
;; US-11-348-413-810033

Query Match 66.3%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACGCGTATCTCTTCAC 19
Db 25 CGCTCGGTATCTCTCTTAC 7

RESULT 19
US-10-511-937-136/c
;; Sequence 136, Application US/10511937
;; Publication No. US20060088836A1
;; GENERAL INFORMATION:
;; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;; APPLICANT: Wollgemuth, Jay
;; APPLICANT: Fry, Kirk
;; APPLICANT: Woodward, Robert
;; APPLICANT: Ly, Ngoc
;; APPLICANT: Prentice, James
;; APPLICANT: Morris, MacDonald
;; APPLICANT: Rosenbery, Steven
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;; FILE REFERENCE: 506612000104
;; CURRENT APPLICATION NUMBER: US/10/511,937
;; CURRENT FILING DATE: 2004-10-19
;; PRIOR APPLICATION NUMBER: PCT/US2003/012946
;; PRIOR FILING DATE: 2003-04-24
;; PRIOR APPLICATION NUMBER: US 10/131,831
;; PRIOR FILING DATE: 2002-04-24
;; PRIOR FILING DATE: 2002-12-20
;; PRIOR APPLICATION NUMBER: US 10/325,899
;; NUMBER OF SEQ ID NOS: 3117
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 136
;; LENGTH: 50
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; US-10-511-937-136

Query Match 66.3%; Score 12.6; DB 6; Length 50;
Best Local Similarity 78.9%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACGCGTATCTCTTCAC 19
Db 49 CTCACGTCTCTCTCTGAC 31

RESULT 20
US-10-554-711-392
;; Sequence 392, Application US/10554711
;; Publication No. US20060115806A1
;; GENERAL INFORMATION:
;; APPLICANT: University of Georgia Research Foundation
;; APPLICANT: McDonald, John F.
;; TITLE OF INVENTION: Global Analysis of Transposable Elements
;; FILE REFERENCE: 21099.0075P1
;; CURRENT APPLICATION NUMBER: US/10/554,711
;; CURRENT FILING DATE: 2005-10-28
;; PRIOR APPLICATION NUMBER: 60/466,798
;; PRIOR FILING DATE: 2003-04-29
;; NUMBER OF SEQ ID NOS: 778
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 392
;; LENGTH: 50
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:/note =
;; OTHER INFORMATION: Synthetic Construct
;; US-10-554-711-392

Query Match 66.3%; Score 12.6; DB 6; Length 50;
Best Local Similarity 78.9%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACGCGTATCTCTTCAC 19
Db 31 CTCACGATCTCTCTTAC 49

RESULT 21
US-11-348-413-257483/c
;; Sequence 257483, Application US/11348413
;; Publication No. US20060160121A1
;; GENERAL INFORMATION:
;; APPLICANT: Wyeth
;; APPLICANT: Mounts, William M
;; APPLICANT: Murphy, Ellen
;; APPLICANT: Olmsted, Stephen
;; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
;; FILE REFERENCE: 031896-084100 (AM 101724)
;; CURRENT APPLICATION NUMBER: US/11/348,413
;; CURRENT FILING DATE: 2006-02-07
;; PRIOR APPLICATION NUMBER: PCT/US05/035471
;; PRIOR FILING DATE: 2005-10-05
;; PRIOR APPLICATION NUMBER: US 11/243,445
;; PRIOR FILING DATE: 2005-10-05
;; PRIOR APPLICATION NUMBER: US 60/615,573
;; PRIOR FILING DATE: 2004-10-05
;; NUMBER OF SEQ ID NOS: 1276209
;; SEQ ID NO 257483
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: probe
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(25)
;; OTHER INFORMATION: SEQ ID NO: 7489; WAN01UMCZ; Start 373; Stop 397;
;; OTHER INFORMATION: 000000011100000
;; US-11-348-413-257483

Query Match 65.3%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ACGGTATCTCTTC 17

Db 17 ACGGTCTCTCTTC 4

RESULT 22

US-11-348-413-257484/c
; Sequence 257484, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 257484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 7489; WANO1UMCZ; Start 374; Stop 398;
; OTHER INFORMATION: 000000011100000
US-11-348-413-257484

Query Match Best Local Similarity 65.3%; Score 12.4; DB 9; Length 25;

Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACGGTATCTCTTC 17
Db 16 ACGGTCTCTCTTC 3

RESULT 23

US-11-348-413-257485/c
; Sequence 257485, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 257485

LENGTH: 25

TYPE: DNA

ORGANISM: Artificial

FEATURE: OTHER INFORMATION: probe

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)-(25)

OTHER INFORMATION: SEQ ID NO: 7489; WANO1UMCZ; Start 375; Stop 399;
; OTHER INFORMATION: 000000011100000
US-11-348-413-257485

Query Match Best Local Similarity 65.3%; Score 12.4; DB 9; Length 25;

Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACGGTATCTCTTC 17
Db 15 ACGGTCTCTCTTC 2

RESULT 24

US-11-348-413-257486/c
; Sequence 257486, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 257486
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 7489; WANO1UMCZ; Start 376; Stop 400;
US-11-348-413-257486

LENGTH: 25

TYPE: DNA

ORGANISM: Artificial

FEATURE: OTHER INFORMATION: probe

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)-(25)

OTHER INFORMATION: SEQ ID NO: 7489; WANO1UMCZ; Start 376; Stop 400;
US-11-348-413-257486

Query Match Best Local Similarity 65.3%; Score 12.4; DB 9; Length 25;

Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACGGTATCTCTTC 17
Db 14 ACGGTCTCTCTTC 1

RESULT 25

US-11-348-413-857440
; Sequence 857440, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445

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; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 857440
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7111; WANO1UMK2_at; Start 619; Stop 643;
; OTHER INFORMATION: 000000011100000
US-11-348-413-857440
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```

Query Match      65.3%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3  ACGGTATCTCTTC 16
         |||||
Db       1  CAAAGTATCTCTTC 14
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```

RESULT 26
US-11-348-413-871598/c
; Sequence 871598, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 871598
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7489; WANO1UMCZ_at; Start 366; Stop 390;
; OTHER INFORMATION: 000000011100000
US-11-348-413-871598
```

```

Query Match      65.3%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      4  ACGGTATCTCTTC 17
         |||||
Db       24  ACGGTCTCTCTTC 11
```

```

RESULT 27
US-11-348-413-871599/c
; Sequence 871599, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
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; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 871599
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7489; WANO1UMCZ_at; Start 371; Stop 395;
; OTHER INFORMATION: 000000011100000
US-11-348-413-871599
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```

Query Match      65.3%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      4  ACGGTATCTCTTC 17
         |||||
Db       19  ACGGTCTCTCTTC 6
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RESULT 28
US-11-240-651-32
; Sequence 32, Application US/11240651
; Publication No. US20060110788A1
; GENERAL INFORMATION:
; APPLICANT: Kudlicki, Wlslaw A.
; APPLICANT: Kerpelipola, Shrantchi
; APPLICANT: Fletcher, Julia
; APPLICANT: Getbehead, Ashley E.
; APPLICANT: Katzen, Federico
; APPLICANT: Voza-Brown, Laura
; TITLE OF INVENTION: Feeding Buffers, Systems, and Methods for In Vitro Synthesis of
; FILE REFERENCE: 0942.6660004
; CURRENT APPLICATION NUMBER: US/11/240,651
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: 60/614,590
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/642,094
; PRIOR FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/656,534
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: Provisional Appl. No. To Be Assigned (Atty. Dkt. No. 0942.66
; 2005-09-27
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BSATA
; OTHER INFORMATION: Chemically synthesized
US-11-240-651-32
```

Query Match	65.3%	Score 12.4	DB 8	Length 31
Best Local Similarity	92.9%	Pred. No. 2.3e+03		
Matches 13	Conservative 0	Mismatches 1	Indels 0	Gaps 0

QY	4	ACGGTATCTCCTTC	17
Db	18	AGGTATCTCCTTC	31

RESULT 29
US-11-240

US-11-240-651-14/c
Sequence 14. Application US/11240651
Publication NO. US20060110788A1
GENERAL INFORMATION:
APPLICANT: Kudlicki, Weislaw A.
APPLICANT: Kępciepola, Shitranchi
APPLICANT: Fletcher, Julia
APPLICANT: Getbehead, Ashley E.
APPLICANT: Katzen, Federico
APPLICANT: Voza-Brown, Laura
TITLE OF INVENTION: Feeding Buffers, Systems, and Methods for In Vitro Synthesis of
TITLE OF INVENTION: Biomolecules
FILE REFERENCE: 0942.666004
CURRENT APPLICATION NUMBER: US/11/240,651
CURRENT FILING DATE: 2005-10-03
PRIOR APPLICATION NUMBER: 60/614,590
PRIOR FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: 60/642,094
PRIOR FILING DATE: 2005-01-10
PRIOR APPLICATION NUMBER: 60/656,534
PRIOR FILING DATE: 2005-02-28
PRIOR APPLICATION NUMBER: Provisional Appl. No. To Be Assigned (Atty. Dkt. No. 0942.6534)
2005-09-27
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.3
SEQ ID NO 14
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: C-Topo2 T7 Promoter
FEATURE:
OTHER INFORMATION: Chemically synthesized
US-11-240-651-14

Query Match	65.3%	Score 12.4;	DB 8;	Length 60;
Best Local Similarity	92.9%;	Pred. No. 2.6e+03;		
Matches 13; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	4	ACGGTATCTCCTTC	17
Db	56	AGGTATCTCCTTC	43

RESULT 30
US-11-348

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; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 429142
; LENGTH: 25

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Query Match	64.2%	Score	12.2	DB	9	Length	25
Best Local Similarity	82.4%	Pred. No.	2.9e+03				
Matches	14	Conservative	0	Mismatches	3	Indels	0
						Gaps	0

QY	2	GCACGGTATCTCCTTCA	18
Db	1	GCAAGATGTTCTCTTCA	17

RESULT 31

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US-11-348-413-636110
/ Sequence 636110, Application US/11348413
/ Publication No. US20060160122A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William M
/ APPLICANT: Murphy, Ellen
/ APPLICANT: Olmsted, Stephen
/ TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
/ FILE REFERENCE: 031896-084100 (AM 101724)
/ CURRENT APPLICATION NUMBER: US/11/348, 413
/ CURRENT FILING DATE: 2006-02-07
/ PRIOR APPLICATION NUMBER: PCT/US05/035471
/ PRIOR FILING DATE: 2005-10-05
/ PRIOR APPLICATION NUMBER: US 11/243, 445
/ PRIOR FILING DATE: 2005-10-05
/ PRIOR APPLICATION NUMBER: US 60/615, 573
/ PRIOR FILING DATE: 2004-10-05
/ NUMBER OF SEQ ID NOS: 1276209
/ SEQ ID NO 636110
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: probe
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)_(25)
/ OTHER INFORMATION: SEQ ID NO: 822; WANO1UJDP_at; Start 908; Stop 932;
/ OTHER INFORMATION: 0111010000000000
US-11-348-413-636110

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Query Match	64.2%	Score 12.2;	DB 9;	Length 25;
Best Local Similarity	82.4%;	Pred. 2.9e+03;		
Matches 14; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

OY		1	CGCACGGTATCTCCCTC	17
Db		4	CGCACGGTATCAACAAC	20

RESULT 32

US-11-348-413-661408/C
; Sequence 661408, Application US/11348413A1
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen

APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 661408
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
NAME/KEY: misc feature
LOCATION: (1)-(25)
OTHER INFORMATION: SEQ ID NO: 1509; WANOIUM2_at; Start 160; Stop 184;
US-11-348-413-661408

Query Match 64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGACGGTATCTCCTTC 17
Db 23 CGAACGATATCGCCTTC 7

RESULT 33
US-11-348-413-661409/c
Sequence 661409, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 661409
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
NAME/KEY: misc feature
LOCATION: (1)-(25)
OTHER INFORMATION: SEQ ID NO: 1509; WANOIUM2_at; Start 162; Stop 186;
US-11-348-413-661409

Query Match 64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGACGGTATCTCCTTC 17
|| ||| ||| ||| ||| ||| |||

Db 21 CGAACGATATCGCCTTC 5

RESULT 34
US-11-348-413-661410/c
Sequence 661410, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 661410
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
NAME/KEY: misc feature
LOCATION: (1)-(25)
OTHER INFORMATION: SEQ ID NO: 1509; WANOIUM2_at; Start 166; Stop 190;
US-11-348-413-661410

Query Match 64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGACGGTATCTCCTTC 17
Db 17 CGAACGATATCGCCTTC 1

RESULT 35
US-11-348-413-701530
Sequence 701530, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 701530
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
NAME/KEY: misc feature

```
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2675; WANO1UN86_at; Start 552; Stop 576;
; OTHER INFORMATION: 1111111000000000
US-11-348-413-701530
```

```
Query Match          64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          3 CACGGTATCTCCTTCAC 19
Db          1 CACGGTAGCTCCTGAC 17
```

```
RESULT 36
US-11-348-413-812478
```

```
; Sequence 812478, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
```

```
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
```

```
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
```

```
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: US/11/348,413
```

```
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
```

```
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
```

```
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
```

```
; SEQ ID NO 812478
```

```
; LENGTH: 25
```

```
; TYPE: DNA
```

```
; ORGANISM: Artificial
```

```
; FEATURE:
```

```
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)..(25)
```

```
; OTHER INFORMATION: SEQ ID NO: 5945; WANO1UUJ4_at; Start 499; Stop 523;
; OTHER INFORMATION: 0000000111000000
US-11-348-413-812478
```

```
Query Match          64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          2 GCACGGTATCTCCTTCA 18
Db          1 GCATGTATGTCTCTCA 17
```

```
RESULT 37
US-11-348-413-90099
```

```
; Sequence 90099, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
```

```
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
```

```
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
```

```
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
```

```
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
```

```
; PRIOR FILING DATE: 2005-10-05
; APPLICANT: Wyeth
```

```
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 90099
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
```

```
; FEATURE:
```

```
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)..(25)
```

```
; OTHER INFORMATION: SEQ ID NO: 2105; WANO1ULANR; Start 922; Stop 946;
; OTHER INFORMATION: 1111111000000000
US-11-348-413-90099
```

```
Query Match          63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          8 TATCTCCTTCAC 19
Db          5 TATCTCCTTCAC 16
```

```
RESULT 38
US-11-348-413-90100
```

```
; Sequence 90100, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
```

```
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
```

```
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
```

```
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: US/11/348,413
```

```
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
```

```
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
```

```
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
```

```
; SEQ ID NO 90100
```

```
; LENGTH: 25
```

```
; TYPE: DNA
```

```
; ORGANISM: Artificial
```

```
; FEATURE:
```

```
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)..(25)
```

```
; OTHER INFORMATION: SEQ ID NO: 2105; WANO1ULANR; Start 923; Stop 947;
; OTHER INFORMATION: 1111111000000000
US-11-348-413-90100
```

```
Query Match          63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          8 TATCTCCTTCAC 19
Db          4 TATCTCCTTCAC 15
```

```
RESULT 39
US-11-348-413-90101
```

```
; Sequence 90101, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
```

```

; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; PRIOR FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 90101
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2105; WANOIUNR; Start 924; Stop 948;
; OTHER INFORMATION: 1111110000000
US-11-348-413-90101

```

```

Query Match      63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 TATCTCCTCACC 19
        |||||
Db       3 TATCTCCTCACC 14

```

```

RESULT 40
US-11-348-413-208705
; Sequence 208705, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 208705
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 6148; WANOIUNR; Start 386; Stop 410;
; OTHER INFORMATION: 000000011100000
US-11-348-413-208705

```

```

Query Match      63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 CGGATCTCCTT 16
        |||||
Db       8 CGGATCTCCTT 19

```

```

Search completed: August 10, 2006, 08:41:55
Job time : 87.6667 secs

```

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 07:10:03 ; Search time 1821.33 Seconds
(without alignments)
583.346 Million cell updates/sec

Title: US-10-636-065-29
Perfect score: 19
Sequence: 1 cgcacgcatcccttcac 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 429206

Minimum DB seq length: 0
Maximum DB seq length: 70

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gsa1:*
12: gb_gsa2:*
13: gb_gsa3:*
14: gb_gsa4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.2	74.7	51	14	LBAP012G02
C 2	13.8	72.6	66	2	BX540068 leishmani
C 3	13.2	69.5	55	1	AA050107 mj10g04.x
C 4	13.2	69.5	55	14	AL767252 Arabidops
C 5	13.2	69.5	68	7	AV833333 AV833333
C 6	12.6	66.3	40	11	AZ489384 1M0321121
C 7	12.6	66.3	62	11	BH000447 2M0288K14
C 8	12.6	66.3	63	2	B1547302 603197180
C 9	12.4	65.3	31	1	AI032171 ou94c11.8
C 10	12.4	65.3	54	11	BZ384637 SALK_1358
C 11	12.4	65.3	66	14	BX946570 Forward s
C 12	12.4	65.3	70	14	CR132014 Arabidops
C 13	12.2	64.2	40	1	AA592106 v014f12.r
C 14	12.2	64.2	41	2	B031518 B031518
C 15	12.2	64.2	54	6	AK219947 Mub muscu
C 16	12.2	64.2	55	1	AA566958 1012 lob1
C 17	12.2	64.2	56	13	CM048735 104_287.1
C 18	12.2	64.2	57	13	CL280533 Ggal_55_V
C 19	12.2	64.2	57	14	CR156504 Forward b

C 20	12.2	64.2	58	1	AA466227	AA466227 vg86h09.x
C 21	12.2	64.2	62	4	CA913895	CA913895 PCS04370
C 22	12.2	64.2	67	1	AA270302	AA270302 v458e05.x
C 23	12.2	64.2	67	1	AA548218	AA548218 n199d10.8
C 24	12.2	64.2	67	10	W36489	W36489 mb71f10.r1
C 25	12	63.2	69	7	BE872737	BE872737 601450859
C 26	11.8	62.1	32	13	C2489694	C2489694 E06954-3P
C 27	11.8	62.1	34	1	AJ662253	AJ662253 AJ662253
C 28	11.8	62.1	34	14	AT769677	AT769677 Arabidops
C 29	11.8	62.1	52	14	ATHS26844	ATHS26844 Arabidops
C 30	11.8	62.1	53	8	CN655993	CN655993 LCM003K_B
C 31	11.8	62.1	55	4	CB006039	CB006039 VWC028H12
C 32	11.8	62.1	62	11	AZ459394	AZ459394 1M0264N10
C 33	11.8	62.1	63	1	AA453052	AA453052 z36f11.x
C 34	11.8	62.1	63	5	CD533428	CD533428 31M20_Ara
C 35	11.8	62.1	65	8	CV305631	CV305631 t164b04.g
C 36	11.8	62.1	65	14	FR0053439	AL689718 Fugu rubr
C 37	11.8	62.1	66	11	BH811036	BH811036 SALK_0571
C 38	11.8	62.1	66	13	BH811037	BH811037 SALK_0571
C 39	11.8	62.1	66	13	CZ012701	CZ012701 BGR574_Ba
C 40	11.8	62.1	68	8	CV305709	CV305709 t164g04.g
C 41	11.8	62.1	68	12	CG538067	CG538067 OST127647
C 42	11.8	62.1	69	11	BH790467	BH790467 SALK_0571
C 43	11.6	61.1	24	5	CF308728	CF308728 ABF--02-K
C 44	11.6	61.1	38	11	BH861410	BH861410 SALK_0815
C 45	11.6	61.1	50	1	AU105011	AU105011 AU105011
C 46	11.6	61.1	50	1	AU105012	AU105012 AU105012
C 47	11.6	61.1	50	1	AU105013	AU105013 AU105013
C 48	11.6	61.1	50	1	AU105014	AU105014 AU105014
C 49	11.6	61.1	50	1	AU105016	AU105016 AU105016
C 50	11.6	61.1	50	1	AU105019	AU105019 AU105019
C 51	11.6	61.1	50	1	AU105021	AU105021 AU105021
C 52	11.6	61.1	50	1	AU105022	AU105022 AU105022
C 53	11.6	61.1	50	1	AU105023	AU105023 AU105023
C 54	11.6	61.1	50	1	AU105024	AU105024 AU105024
C 55	11.6	61.1	50	1	AU105025	AU105025 AU105025
C 56	11.6	61.1	50	1	AU105026	AU105026 AU105026
C 57	11.6	61.1	50	1	AU105028	AU105028 AU105028
C 58	11.6	61.1	50	1	AU105030	AU105030 AU105030
C 59	11.6	61.1	50	1	AU105031	AU105031 AU105031
C 60	11.6	61.1	50	1	AU105032	AU105032 AU105032
C 61	11.6	61.1	50	1	AU105033	AU105033 AU105033
C 62	11.6	61.1	50	1	AU105035	AU105035 AU105035
C 63	11.6	61.1	50	1	AU105036	AU105036 AU105036
C 64	11.6	61.1	50	1	AU105037	AU105037 AU105037
C 65	11.6	61.1	50	1	AU105038	AU105038 AU105038
C 66	11.6	61.1	50	1	AU105039	AU105039 AU105039
C 67	11.6	61.1	50	1	AU105040	AU105040 AU105040
C 68	11.6	61.1	50	1	AU105041	AU105041 AU105041
C 69	11.6	61.1	50	1	AU105042	AU105042 AU105042
C 70	11.6	61.1	50	1	AU105043	AU105043 AU105043
C 71	11.6	61.1	50	1	AU105044	AU105044 AU105044
C 72	11.6	61.1	50	1	AU105047	AU105047 AU105047
C 73	11.6	61.1	50	1	AU105048	AU105048 AU105048
C 74	11.6	61.1	50	1	AU105050	AU105050 AU105050
C 75	11.6	61.1	50	1	AU105052	AU105052 AU105052
C 76	11.6	61.1	50	1	AU105054	AU105054 AU105054
C 77	11.6	61.1	50	1	AU105055	AU105055 AU105055
C 78	11.6	61.1	50	1	AU105059	AU105059 AU105059
C 79	11.6	61.1	50	1	AU105060	AU105060 AU105060
C 80	11.6	61.1	50	1	AU105064	AU105064 AU105064
C 81	11.6	61.1	50	1	AU105068	AU105068 AU105068
C 82	11.6	61.1	50	1	AU105069	AU105069 AU105069
C 83	11.6	61.1	50	1	AU105071	AU105071 AU105071
C 84	11.6	61.1	50	1	AU105072	AU105072 AU105072
C 85	11.6	61.1	50	1	AU105076	AU105076 AU105076
C 86	11.6	61.1	50	1	AU105077	AU105077 AU105077
C 87	11.6	61.1	50	1	AU105080	AU105080 AU105080
C 88	11.6	61.1	50	1	AU105085	AU105085 AU105085
C 89	11.6	61.1	50	1	AU105087	AU105087 AU105087
C 90	11.6	61.1	50	1	AU105088	AU105088 AU105088
C 91	11.6	61.1	50	1	AU105089	AU105089 AU105089
C 92	11.6	61.1	50	1	AU105090	AU105090 AU105090

c 93 11.6 61.1 50 1 AUI05092 AUI05092 AUI05092
 c 94 11.6 61.1 50 1 AUI05093 AUI05093 AUI05093
 c 95 11.6 61.1 50 1 AUI05094 AUI05094 AUI05094
 c 96 11.6 61.1 50 3 BP132714 BP132714 BP132714
 c 97 11.6 61.1 55 10 T57237 T57237 yb21h06.t1
 c 98 11.6 61.1 62 10 DR368321 DR368321 6630667 C
 c 99 11.6 61.1 64 1 A119176 A119176 q576d08.x
 c 100 11.6 61.1 64 11 B07692 B07692 CDC9f10 C-1

ALIGNMENTS

RESULT 1
 LBAF012G02/c 51 bp DNA linear GSS 20-JUN-2003
 LOCUS LBAF012G02
 DEFINITION Leishmania braziliensis GSS, clone LBAF012G02, genomic survey
 sequence.

ACCESSION BX540068 GI:32135483
 VERSION BX540068.1 GI:32135483
 KEYWORDS GSS; genomic survey sequence.
 SOURCE Leishmania braziliensis
 ORGANISM Leishmania braziliensis
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Leishmania; Leishmania braziliensis species complex.

REFERENCE 1
 AUTHORS Laurentino,E.C., Ruiz,J.C. and Cruz,A.K.
 TITLE GSS analysis of the Leishmania braziliensis genome
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 51)
 AUTHORS Cruz,A.K.
 TITLE Direct Submission

COMMENT Submitted (17-JUN-2003) Cruz A.K., University of Sao Paulo,
 Department of Molecular and Cell Biology, FMRP, Avenida
 Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL

FEATURES
 Location: akcruz@fmrp.usp.br.
 source

1.51
 /organism="Leishmania braziliensis"
 /mol_type="genomic DNA"
 /strain="MHOM/BR/75/M2904"
 /db_xref="taxon:5660"
 /clone="LBAF012G02"

ORIGIN

Query Match 74.7%; Score 14.2; DB 14; Length 51;
 Best Local Similarity 84.2%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTCAC 19
 |||||
 32 CGCAGCGTATCTCCTTCAC 14

Db

RESULT 2
 BI218136/c 66 bp mRNA linear EST 11-JUL-2001
 LOCUS BI218136
 DEFINITION 602934250F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5097541 5',
 mRNA sequence.

ACCESSION BI218136 GI:14671580
 VERSION BI218136
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidae; Muridae; Murinae; Mus.

1 (bases 1 to 66)

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs-r@mail.nih.gov

FEATURES

Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 plate: LLM11234 row: c column: 14
 High quality sequence stop: 64.
 Location/Qualifiers

1..66
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5097541"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_11b="NCI CGAP_L19"
 /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP library."

ORIGIN

Query Match 72.6%; Score 13.8; DB 2; Length 66;
 Best Local Similarity 88.2%; Pred. No. 2.3e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTC 17
 |||||
 Db 24 CGCAGCGTATCTCCTTC 8

RESULT 3

AA050107 55 bp mRNA linear EST 09-SEP-1996
 LOCUS AA050107
 DEFINITION mJ10904.t1 Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA
 clone IMAGE:475734 5' similar to SW:WPS1_HUMAN P42677
 MERRILOPAN-STIMULIN 1, mRNA sequence.

ACCESSION AA050107 GI:1529795
 VERSION AA050107.1 GI:1529795
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 55)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

The WashU-HMNI Mouse EST Project
 Unpublished (1996)
 CONTACT: Marra M/Mouse EST Project
 WashU-HMNI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

JOURNAL

COMMENT

Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:286478

Trice considered overall poor quality
 Possible reversed clone; similarity on wrong strand
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

1..55
 /organism="Mus musculus"
 /mol_type="mRNA"

Best Local Similarity 83.3%; Pred. No. 4.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GCACGGATCTCTTCAC 19
Db 30 GCGCGATATCCTTCAC 13

RESULT 6
AZ489384/c 40 bp DNA linear GSS 05-OCT-2000

LOCUS 1M0321121F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0321121 F, genomic survey sequence.

ACCESSION AZ489384

VERSION AZ489384.1 GI:10659081

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 40)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0321 row: 1 column: 21
Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends
High quality sequence stop: 40.

Location/Qualifiers

1. 40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0321121"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 66.3%; Score 12.6; DB 11; Length 40;
Best Local Similarity 78.9%; Pred. No. 9.6e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGACGGATCTCTTCAC 19
Db 33 CACAGGATATCTCTTCAC 15

RESULT 7

BH000447/c

LOCUS 2M0288K14F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0288K14 F, genomic survey sequence.

ACCESSION BH000447

VERSION BH000447.1 GI:13871673

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 62)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0288 row: K column: 14
Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends
High quality sequence stop: 62.

Location/Qualifiers

1. 62
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0288K14"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 66.3%; Score 12.6; DB 11; Length 62;
 Best Local Similarity 78.9%; Pred. No. 1e+05; 4; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTCAC 19
 |||||
 45 CACCCAGTCTCTCCTTCAC 27

RESULT 8
 B1547302/c 63 bp mRNA linear EST 05-SEP-2001
 LOCUS 603197180F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5276803 5',
 DEFINITION mRNA sequence.
 ACCESSION B1547302
 VERSION B1547302
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 63)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NIGRI), Shitaki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: LLAM1698 row: p column: 20
 High quality sequence stop: 9.
 Location/Qualifiers
 1. 63
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5276803"
 /rname="hippocampus"
 /lab_host="DH10B"
 /clone_lib="NIH MGC_95"
 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
 (gtagg); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.5 kb and normalized to R0T 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIGRI/NIGRI, National Institutes of Health). Note: this
 is a NIH_MGC library."

ORIGIN

Query Match 66.3%; Score 12.6; DB 2; Length 63;
 Best Local Similarity 78.9%; Pred. No. 1e+05; 4; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTCAC 19
 |||||
 43 CGCAGCTTAGGCCCTTCAC 25

RESULT 9
 A1032171 31 bp mRNA linear EST 27-AUG-1998
 LOCUS 0094611.01 NCI_CGAP_kid3 Homo sapiens cDNA clone IMAGE:1635476 3',
 DEFINITION

similar to SW:PFOX_HUMAN P50336 PROTOPORPHYRINOGEN OXIDASE ;, mRNA
 sequence.
 A1032171
 A1032171.1 GI:3250383
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 31)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bdrip/image/image.html

Trace considered overall poor quality
 Insert Length: 1676 Std Error: 0.00
 Seq primer: -40ml3 fwd. RT from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 31
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1635476"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP_kid3"
 /note="Organ: Kidney; Vector: p773D-PacI, Site_1: Not I;
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer, double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified p773
 vector. mRNA source: 2 pooled kidneys. Library went
 through one round of normalization. Library constructed by
 Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 65.3%; Score 12.4; DB 1; Length 31;
 Best Local Similarity 92.9%; Pred. No. 1.2e+05; 1; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCA 18
 |||||
 2 CGGATCTCCTTCA 15

RESULT 10
 B2384637/c 54 bp DNA linear GSS 26-NOV-2002
 LOCUS SALK_135814.20.40.x Arabidopsis thaliana TDNA insertion lines
 DEFINITION Arabidopsis thaliana genomic clone SALK_135814.20.40.x, genomic
 survey sequence.
 ACCESSION B2384637
 VERSION B2384637
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 54)
 Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R.,

TITLE
A Sequence-indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL
Unpublished (2001)

COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5g06840.
Class: TDNA tagged.

FEATURES

source

1..54
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_135814.20.40.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match
Best Local Similarity 92.3%; Score 12.4; DB 11; Length 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGTATCTCCTT 16
|||||
50 CACGGTATCACCCT 37

Db

RESULT 11
CRI32014 66 bp DNA linear GSS 06-JUL-2004
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN363121, genomic survey sequence.
ACCESSION CRI32014
KEYWORDS CRI32014.1 GI:49879467
SOURCE GSS; genome survey sequence; MICEP.
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Mus musculus
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 66)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.

TITLE
JOURNAL Direct Submision
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. <http://www.sanger.ac.uk/MICEP>

FEATURES

source

1..66
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN363121"
/clone_lib="MHPN"

ORIGIN

Query Match
Best Local Similarity 92.9%; Score 12.4; DB 14; Length 66;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGTATCTCTTCAC 19
|||||
Db 21 GGTATCTCTTCAC 34

RESULT 12
BX946520 70 bp DNA linear GSS 05-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GR-767D03-024595,
DEFINITION genomic survey sequence.
ACCESSION BX946520
KEYWORDS BX946520.1 GI:42596206
SOURCE GSS.
ORGANISM Arabidopsis thaliana (thale cress)

REFERENCE

AUTHORS

TITLE

JOURNAL
PUBMED Arabidopsis thaliana T-DNA flanking sequence tag (PST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana Bioinformatics 19 (11), 1441-1442 (2003)
12874060

REFERENCE
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reis,B., Dekker,K. and Weishaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321

TITLE
JOURNAL
PUBMED High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050

REFERENCE
AUTHORS Rosso,M.G., Strizhov,N., Li,Y. and Weishaar,B.
Direct Submision
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
14682050

COMMENT

It indicates an insertion within the locus defined by BAC clone fish18. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1..70
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-767D03-024595"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match
Best Local Similarity 92.3%; Score 12.4; DB 14; Length 70;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY	1	CGACGGATCTCC	14
DB	29	CGACGGATCTTC	16
RESULT 13			
AA592106/c			
LOCUS			
DEFINITION	AA592106	40 bp	mRNA EST 17-SEP-1997
ACCSSION	U04112.r1	Barstead mouse myotubes MRLR5	Mus musculus cDNA clone
VERSION	IMAGE:1049903 5'	similar to TR.G299054 G299054 SC56=SYNAFTONEMAL	
KEYWORDS	COMPLEX PROTEIN . ;	mRNA sequence.	
SOURCE	AA592106		
ORGANISM	AA592106.1	GI:2405769	
REFERENCE	EST.		
AUTHORS	Mus musculus (house mouse)		
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
COMMENT	Sciurognathi; Murioidea; Muridae; Murinae; Mus.		
	1 (bases 1 to 40)		
	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,		
	Giesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,		
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,		
	Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and		
	Waterston,R.		
	The WashU-HM Mouse EST Project		
	Unpublished (1996)		
	Contact: Marra M/Mouse EST Project		
	WashU-HM Mouse EST Project		
	Washington University School of MedicineP		
	4444 Forest Park Parkway, Box 850L, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: mouseest@watson.wustl.edu		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	MG1:581479		
	Trace considered overall poor quality		
	Possible reversed clone; similarity on wrong strand		
	Seq primer: -28mJ rev2 ET from Amersham		
	High quality sequence stop: 1.		
FEATURES			
SOURCE			
	Location/Qualifiers		
	1..40		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/strain="C3H"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:1049903"		
	/cell_line="C2C12"		
	/lab_host="DH10B"		
	/clone_lbb="Barstead mouse myotubes MRLR5"		
	/note="Vector: pRTT3D-PacI; Site_1: EcoRI; Site_2: NotI;		
	1st strand cDNA was primed with a Not I - oligo(dT) primer		
	'5,		
	TTTAAGCATCTGAAGTGAGCGGCGCCCTTTTTTTTTTTTTTTTTTTTTT		
	3']; double-stranded cDNA was ligated to Eco RI adaptors		
	(AATTGGATCCTTG), digested with Not I and cloned into the		
	Not I and Eco RI sites of the modified pRTT3 vector.		
	Library constructed by Bob Barstead. The C2C12 cell line		
	(available from ATCC, catalog # CRL-1772) differentiates		
	rapidly, forming contractile myotubes and producing		
	characteristic muscle proteins.		
ORIGIN			
Query Match	64.2%	Score 12.2;	DB 1; Length 40;
Best Local Similarity	82.4%;	Pred. No. 1.6e+05;	
Matches 14;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;
1	CGACGGATCTCC	17	
30	CGACAGTTGCCTTC	14	

```

RESULT 14
B0031518/c 41 bp mRNA EST 26-SEP-2003
LOCUS
DEFINITION
B0031518 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL007109 5', mRNA sequence.
B0031518
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 41)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and
Kohara,Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@gene.nig.ac.jp
The information of this clone is available through the following
URL.
http://xenopus.nibb.ac.jp.
location/qualifiers
1..41
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL007109"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/clone_id="NIBB Mochii normalized Xenopus neurula
library"

ORIGIN
Query Match 64.2%; Score 12.2; DB 2; Length 41;
Best Local Similarity 77.8%; Pred. No. 1.66+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CGCAGCGATCTCCTTCA 18
24 CGCCTATATCTCTCCA 7

RESULT 15
AK219947 54 bp mRNA linear HTC 23-NOV-2004
LOCUS
DEFINITION
Mus musculus cDNA, clone:Y2G0150D19, strand:unspecified.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
Watabiki,A., Waki,K., Hayatsu,N., Shiraki,T., Kondo,S.,
Nakamura,M., Sasaki,D., Arakawa,T., Kawai,J., Harbers,M.,
Hayashizaki,Y. and Carninci,F.
Libraries enriched for alternatively spliced exons reveal splicing
patterns in melanocytes and melanomas
Nat. Methods 1, 233-239 (2004)
2 (bases 1 to 54)
Arakawa,T., Carninci,F., Fukuda,S., Harbers,M., Hayatsu,N.,
Hoti,F., Imotani,K., Kawai,J., Kondo,S., Murata,M., Nakamura,M.,
Nomura,K., Ohno,M., Sasaki,D., Shiraki,T., Waki,K., Watabiki,A. and
Hayashizaki,Y.

```

TITLE	Direct Submission									
JOURNAL	Submitted (15-SEP-2004) Yoshitake Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsukuba-Ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp, Tel:81-45-503-9222, Fax:81-45-503-9216)									
COMMENT	Alternative Splicing Libraries (ASLs) are prepared by: Preparing of single-stranded DNA using a RNA template from full length cDNA libraries, hybridizing of single-stranded DNAs, removing of remaining single-stranded DNA, digesting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligation of Y-shaped primers to isolated DNA hybrids with loop structures, PCR amplification of ligation products and their cloning into pFIC1 vector. (Reference) .									
FEATURES	location/Qualifiers									
source	1..54									
	/organism="Mus musculus"									
	/mol_type="mRNA"									
	/db_xref="taxon:10090"									
	/clone="Y2G0150D19"									
	/cell_line="mixture of B16-F10Y and melan-c"									
	/cell_type="mixture of melanoma cell and melanocyte cell"									
	/clone_lib="Alternative Splicing Library L3"									
	/note="strand:unspecified"									
ORIGIN										
Query Match	64.2%	Score 12.2;	DB 6;	Length 54;						
Best Local Similarity	82.4%	Pred. No. 1.6e+05;								
Matches 14;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;						
QY	1	CGCAGGATCTCCTTC	17							
Db	21	CCGAGATCTCCTTC	37							
RESULT 16										
LOCUS	AA566958	55 bp	mRNA	linear	EST 28-AUG-1998					
DEFINITION	1012 loblolly pine C Pinus taeda cDNA clone 5c6g, mRNA sequence.									
ACCESSION	AA566958									
VERSION	AA566958.1	GI:3366171								
KEYWORDS	EST.									
SOURCE	Pinus taeda (loblolly pine)									
ORGANISM	Pinus taeda									
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 55)									
REFERENCE	Allona, I., Quim, M., Shoop, E., Swope, K., St. Cyr, S., Carlis, J., Riedl, J., Retzel, E., Campbell, M.M., Sedoreff, R. and Whetten, R.W. Analysis of xylem formation in pine by cDNA sequencing									
TITLE	Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9693-9698 (1998)									
JOURNAL	9699143									
PUBMED	Contact: Ross Whetten									
COMMENT	Forest Biotechnology Group									
	North Carolina State University									
	Dept. of Forestry, NC State University, 6113 Jordan Hall,									
	Raleigh, NC, 27695-8008									
	Tel: 919-515-7800									
	Fax: 919-515-7801									
	Email: rosswhet@unity.ncsu.edu									
	Seq primer: T3.									
FEATURES	location/Qualifiers									
source	1..55									
	/organism="Pinus taeda"									
	/mol_type="mRNA"									
	/strain="Coastal plain loblolly pine from North Carolina"									
	/db_xref="taxon:3352"									
	/clone="5c6g"									
	/issue_type="Xylem"									
	/lab_host="SOIR"									

		/clone_lib="roblojly pine C"
		/note=Vector: lambda-ZAP; Site_1: EcoRI; Site_2: XhoI;
		The library was made from immature xylem from The
		underside of inclined stems of differentiating wood. A
		mixture of four genotypes were used. Oligo-dT prime cDNA
		was directionally cloned into the EcoRI-XhoI lambda-ZAP
		vector arms"
ORIGIN		
Query Match	64.2%; Score 12.2; DB 1; Length 55;	
Best Local Similarity	77.8%; Pred. No. 1.6e+05;	
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
Dn	2 GCACGGATCTCCTTCAC 19 36 GCAGGCGATTNCTTCAC 53	
RESULT_17		
CW048735		
LOCUS		
DEFINITION	104,287,10513599..115,30213 Sorghum methylation filtered library (libid: 104) Sorghum bicolor genomic clone 10513599, genomic survey sequence.	
ACCESSION	CW048735	
VERSION	GSS.	
KEYWORDS	Sorghum bicolor (Sorghum)	
SOURCE	Sorghum bicolor	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum. 1 (bases 1 to 56) Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,B., Rohlfing,T., Fries,J., Bradford,K., McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korfi,I.F., Radinowicz,P.D., Lakey,N., McCormick,W.R., Jeddelson,V.A. and Martienssen,R.A. Sorghum genome sequencing by methylation filtration PLoS Biol. 3 (1), e13 (2005) 15660154	
REFERENCE	Contact: Bedell JA Orion Genomics, LLC 4041 Forest Park Ave, St. Louis, MO 63108, USA Tel: 314 615 6979 Fax: 314 615 5975 Email: jbedell@oriongenomics.com Plate: 287 row: J column: 13 Seq primer: M13/pUC Reverse Class: methylation filtered High quality sequence stop: 56. Location/Qualifiers	
AUTHORS	1. 56	
JOURNAL PUBMED	/organism="Sorghum bicolor" /mol_type="genomic DNA" /cultivar="ATx623" /db_xref="taxon:4558" /clone="10513599" /_clone_lib="Sorghum methylation filtered library (libid: 104)"	
TITLE COMMENT	_note="Organ: leaf; Vector: pBSCSK(-); Site_1: HincII, DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HindIII-digested pBSCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."	
FEATURES		
source		
ORIGIN		
Query Match	64.2%; Score 12.2; DB 13; Length 56;	
Best Local Similarity	82.4%; Pred. No. 1.6e+05;	
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
Dn	1 CGCACGGTATCTCCCTTC 17	

[illegible]

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JOURNAL      Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
FEATURES     CB10 ISA, UK http://www.sanger.ac.uk/MICER
SOURCE       Location/Qualifiers
            1..57
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /db_xref="taxon:10090"
                /clone="MHP17121"
                /clone_lib="MHP"

ORIGIN
Query Match      64.2%; Score 12.2; DB 14; Length 57;
Best Local Similarity 82.4%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 GCACGATATCTCCTCA 18
          ||| ||| ||| ||| |||
Db      57 GCGCGATCTCCATCA 41

RESULT 20
LOCUS      AA466227
DEFINITION
AA466227          58 bp      mRNA      linear      EST 11-JUN-1997
v86bh09.r1 Barstead mouse pooled organs MPRB4 Mus musculus cDNA
clone IMAGE:872897 5' similar to SWUCQ_BOVIN P13271
UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN
QP-C ;, mRNA sequence.
AA466227
AA466227.1 GI:2192367
EST.
Mus musculus (house mouse)
Mus musculus
Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteleostomi; Euteleostomi; Euteleostomi; Euteleostomi;
Sciurognathi; Muridae; Muridae; Muridae; Muridae; Muridae; Mus.
1 (bases 1 to 58)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Teisberg, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:512377
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 BT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
            1..58
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:872897"
                /sex="mixed"
                /tissue_type="pooled organs"
                /dev_stage="7 day"
                /lab_host="DH10B"
                /clone_lib="Barstead mouse pooled organs MPRB4"
                /notes="Organ: pooled; Vector: pRTT3-Pac1; Site 1: BcORI;
                Site 2: NotI; 1st strand cDNA was primed with a Not I -
                oligo(dT) primer [5
                TGTTAGCAATCTGAAGTGAGGAGCGCGCCGCTTTTTTTTTTTTTTTTTTTTTTTT

```

3'] : double-stranded cDNA was ligated to Eco RI adaptors [GTGATTCGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed by Bob Barstead."

ORIGIN

Query Match 64.2%; Score 12.2; DB 1; Length 58;
 Best Local Similarity 82.4%; Pred. No. 1.7e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 31 GCACGATCTCCTTCA 18
 31 GCACGATCTCCTTCA 47

RESULT 21

CA913895 62 bp mRNA linear EST 27-DEC-2002
 LOCUS PCS04370 Scarlet Runner Bean Susensor Region Triplex2 Phaseolus
 DEFINITION coccineus cDNA 5' similar to sc07b11.y1 Gm-cl035 Glycine max cDNA,
 mRNA sequence.

ACCESSION CA913895 GI:27400887
 VERSION CA913895
 KEYWORDS EST.
 SOURCE Phaseolus coccineus
 ORGANISM Phaseolus coccineus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Phaseolus.
 1 (bases 1 to 62)
 Bul, A.O., Le, B.H., Weterings, K., Bi, Y.-P., Choi, J.-S.,
 McElroy, K.E., Choi, P.S., Harada, J.J., Fischer, R.L. and
 Goldberg, R.B.

REFERENCE

Gene Activity in Different Regions of a Post-Fertilization Plant
 Embryo by EST Analysis
 Unpublished (2002)

TITLE

JOURNAL

COMMENT

Contact: Goldberg, R.B.
 Department of Molecular, Cell, & Developmental Biology
 University of California, Los Angeles
 621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA
 Tel: 310 825 3270
 Fax: 310 825 3270
 Email: bob@ucla.edu
 Seq primer: 5' Triplex
 POLYA=No.

FEATURES

source

1..62 Location/Qualifiers
 /organism="Phaseolus coccineus"
 /mol_type="mRNA"
 /cultivar="Hammond's Dwarf Scarlet"
 /db_xref="taxon:3886"
 /dev_stage="6-days post-pollination"
 /clone_lib="Scarlet Runner Bean Susensor Region Triplex2"
 /note="Organ: Susensor Region of Global-Stage Embryos;
 Vector: Triplex2; Site 1: SfiIA; Site 2: SfiIB; Susensor
 regions were micro-dissected from global-stage embryos
 six days after pollination from greenhouse-grown plants
 [Weterings et al., Plant Cell 13, 2409-2425 (2001)].
 Double-stranded cDNA was synthesized from susensor mRNA
 using the SMART cDNA Library Construction Kit according to
 the manufacturer (Clontech). The susensor cDNA fragments
 were directionally ligated into the SfiI restriction site
 of the lambda Triplex2 vector (Clontech), and the
 recombinant cDNAs were transformed into E. coli XL1-Blue
 cells (Clontech). Susensor cDNA plasmids used for
 directional sequencing were obtained by in vivo excision
 from the lambda Triplex2 recombinants in E. coli BM25.8
 cells (Clontech)."

ORIGIN

Query Match 64.2%; Score 12.2; DB 4; Length 62;
 Best Local Similarity 82.4%; Pred. No. 1.7e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 CACGATCTCCTTCA 19
 12 CACGATCTCCTTCA 28

Db

RESULT 22

AA270302 67 bp mRNA linear EST 26-MAR-1997
 LOCUS AA270302
 DEFINITION vasc05.r1 Soares mouse 3NME12.5 Mus musculus cDNA clone
 IMAGE:735584 5' similar to SW:UCRO BOVIN P13271
 UB1QUINOL-CYTOCHROME C REDUCTASE COMPLEX UB1QUINONE-BINDING PROTEIN
 OP-C ; mRNA sequence.

ACCESSION AA270302 GI:1908666
 VERSION AA270302
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE

Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 67)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Stepcoe, M., Tan, F., Underwood, K., Moore, B.,
 Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu

TITLE

JOURNAL

COMMENT

This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:452632
 Trace considered overall poor quality
 Possible reversed clone; similarity on wrong strand
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 1.

FEATURES

source

1..67 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:735584"
 /sex="unknown"
 /tissue_type="fetus"
 /dev_stage="12.5dpc total fetus"
 /lab_host="DH10B"
 /clone_lib="Soares mouse 3NME12.5"
 /note="Organ: whole fetus; Vector: pT73D-PacI; Site 1:
 Not I; Site 2: Eco RI; 1st strand cDNA was primed with a
 Not I - oligo(dT) primer [5'
 TGTTCACATCTGAAGTGGAGCGCGCTTATTTTTTTTTTTTTTTT 3'] ,
 on total mouse RNA [provided by Minoru Ko, Wayne State
 Univ.]; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT73 vector.
 Library went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 64.2%; Score 12.2; DB 1; Length 67;
 Best Local Similarity 82.4%; Pred. No. 1.7e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 GCACGATCTCCTTCA 18

Db 31 GCACGATCTCTTCA 47

RESULT 23
AA548218/c
LOCUS
DEFINITION
AA548218 67 bp mRNA linear EST 05-SEP-1997
nj99d10.61 NCI CGAP Pr11 Homo sapiens CDNA clone IMAGE:1000627
similar to GB:M2125 TROPOMYOSIN, FIBROBLAST AND EPITHELIAL
MUSCLE-TYPE (HUMAN);, mRNA sequence.

ACCESSION
AA548218
VERSION
AA548218.1 GI:2318500
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS
TITLE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
Chuacui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bdrp/image/image.html

FEATURES
source
Trace considered overall poor quality
Insert Length: 585 Std Error: 0.00
Seq primer: -40m13 fwd. 5' from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..67
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1000627"
/sex="male"
/tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"
/clone_id="NCI CGAP Pr11"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells; cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. Library made by
D. Krizman, NIH."

ORIGIN
Query Match 64.2%; Score 12.2; DB 1; Length 67;
Best Local Similarity 82.4%; Pred. No. 1.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGCATCTCTTC 17
Db 38 GCACCGACGATCTCTTC 22

RESULT 24
W36489
LOCUS
DEFINITION
W36489 67 bp mRNA linear EST 12-SEP-1996
mb71f10.r1 Soares mouse p3MP19.5 Mus musculus cDNA clone
IMAGE:334891 5' similar to SW:UCR7 BOVIN P13271
UBQUINOL-CYTOCROME C REDUCTASE 9.5 KD PROTEIN ;, mRNA sequence.
W36489
VERSION
W36489.1 GI:1318394
KEYWORDS
EST.

SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
TITLE
The WashU-HMI Mouse EST Project
JOURNAL
COMMENT
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:216291

FEATURES
source
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..67
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:334891"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_id="Soares mouse p3MP19.5"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACCACTGAGAGTGGAGCGCGCATTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."

ORIGIN
Query Match 64.2%; Score 12.2; DB 10; Length 67;
Best Local Similarity 82.4%; Pred. No. 1.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGATCTCTTCA 18
Db 31 GCACGATCTCTTCA 47

RESULT 25
BE872737
LOCUS
DEFINITION
BE872737 69 bp mRNA linear EST 20-OCT-2000
601450859F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854607 5',
mRNA sequence.
BE872737
VERSION
BE872737.1 GI:10321513
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>
 Plate: LHM9580 row: 6 column: 16
 High quality sequence stop: 69.

FEATURES

source

```
1..69
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGR:3854607"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_idb="NH_MGC_65"
/note="Organ: colon; Vector: PCMV-SPORT6; Site_1: NotI, Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."
```

ORIGIN

Query Match 63.2%; Score 12; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GATCTCTCTTCA 18
 |||||
 Db 23 GATCTCTTCA 34

RESULT 26 32 bp DNA linear GSS 29-APR-2005
 C2489694/f06954-prime Exelixis piggyBac WH insertions Drosophila melanogaster genomic Sequence recovered from 3' end of piggyBac, genomic survey sequence.
 C2489694
 C2489694.1 GI:62987132

ACCESSION C2489694
VERSION C2489694
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 32)

AUTHORS

Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.D., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Greer, K., Hartouni, S.R., Howie, B., Jakkula, L., Joo, D., Kilpatrick, K., Laufer, A., Mazotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Tan, L.R., Ventura, R., Woo, A., Zakrzewski, I., Zhao, L., Chen, F., Swimmer, C., Koczynski, C., Duyk, G., Winberg, M.L. and Margolis, J.
 A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac
 Nat. Genet. 36 (3), 283-287 (2004)
 14981521

JOURNAL

PUBLISHED 14981521

COMMENT

Contact: Roger A Hoskins
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
 Tel: 510 486 4015
 Fax: 510 486 6798
 Email: Rhoskins@lbl.gov
 Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of piggyBac element.

The piggyBac insertion position is 1 in the 32 bases. This insertion position refers to the first base of the 4 base TAA target recognition sequence.
 Class: transposon insertion site.
 Location/Qualifiers

FEATURES

source

```
1..32
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_idb="Exelixis piggyBac WH insertions"
/note="Vector: piggyBac WH (GenBank accession number AY515148); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the WH element using the constitutive alpha-1 tubulin-piggyBac transposase source. We remobilized the WH element from a single amniation element on the Biminscy balancer chromosome in dysgenic females. We outcrossed dysgenic virgin females in vials to the isogenic w- strain and selected new hops in the following generation. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."
```

ORIGIN

Query Match 62.1%; Score 11.8; DB 13; Length 32;
Best Local Similarity 86.7%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 ACGGTATCTCTTCA 18
 |||||
 Db 31 ACGGTATTTCTTCA 17

RESULT 27 34 bp mRNA linear EST 28-JUN-2004
 AJ662253
 AJ662253 CSEQRAN09 Sus scrofa cDNA clone C0000023_F16, mRNA sequence.

ACCESSION AJ662253
VERSION AJ662253.1 GI:49346376
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Sus.
 1 (bases 1 to 34)

Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
 Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
 Unpublished (2004)

AUTHORS

JOURNAL Roslin Institute
 Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross-match with the -minscore 20 and -mismatch 12 options. Vector: pBluescriptII (KS+). R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentae. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
 Location/Qualifiers

FEATURES

source

```
1..34
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000023_F16"
/tissue_type="placenta"
/clone_idb="CSEQRAN09"
/note="Vector: pBluescriptII (KS+); Site_1: EcoRI; Site_2:
```


NotI, Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

Query Match 62.1%; Score 11.8; DB 1; Length 34;
Best Local Similarity 86.7%; Pred. No. 2.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 62.1%; Score 11.8; DB 14; Length 34;
Best Local Similarity 86.7%; Pred. No. 2.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 CGGTATCTCCTTCC 19
|||||
Db 10 CGGTTCCTTCAC 24

OY 5 CGGTATCTCCTTCC 19
|||||
Db 13 CGGTTCCTTCACC 27

RESULT 28

AL769677 34 bp DNA linear GSS 01-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-091A08-011956,
DEFINITION genomic survey sequence.
ACCESSION AL769677
VERSION AL769677.1 GI:21531879
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

RESULT 29
ATH526844/c 52 bp DNA linear GSS 08-FEB-2006
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 127H07, genomic survey sequence.
ACCESSION AJ526844
VERSION AJ526844.1 GI:26795104
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321

REFERENCE
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, P., Chauvin, S., Bechtold, N., Crnaud, C., DeRose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
AUTHORS Balzerque, S.
TITLE Direct Submision
COMMENT Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12446565
AUTHORS Balzerque, S.
TITLE Direct Submision
COMMENT Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

REFERENCE
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weishaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
AUTHORS Rosso, M.G., Li, Y., Strizhov, N. and Weishaar, B.
TITLE Direct Submision
COMMENT Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone K19E1. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpi-koein.mpg.de/GABI-Kat/>.

FEATURES
source location/Qualifiers
1..34
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-091A08-011956"
/clone_1fb="Arabidopsis thaliana T-DNA insertion lines"
/clone_2fb="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pACT161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced

FEATURES
source location/Qualifiers
1..52
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassilewskija"
/db_xref="taxon:3702"
/clone="127H07"
/clone_1fb="Arabidopsis thaliana T-DNA insertion lines"
/clone_2fb="Wassilewskija"
misc_feature 1..53
/notes="T-DNA flanking sequence left border"

ORIGIN
Query Match 62.1%; Score 11.8; DB 14; Length 52;
Best Local Similarity 86.7%; Pred. No. 2.7e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 ACCGATCTCTTCA 18
|||||
Db 28 ACTGATCTGCTTCA 14

ORIGIN
Query Match 62.1%; Score 11.8; DB 1; Length 34;
Best Local Similarity 86.7%; Pred. No. 2.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 ACCGATCTCTTCA 18
|||||
Db 28 ACTGATCTGCTTCA 14

```

RESULT 30
CN655993
LOCUS
DEFINITION LCM003K_B04_T3_D04_04 LCM003 library Glycine max cDNA 5', mRNA
sequence.
ACCESSION CN655993
VERSION
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 53)
Klink,V.P., Alharouf,N.W., Macdonald,M. and Matthews,B.F.
Laser Capture Microdissection (LCM) and Expression Analyses of
Glycine max (Soybean) Syncytium Containing Root Regions Formed by
the Plant Pathogen Heterodera glycines (Soybean Cyst Nematode)
Plant Mol Biol. 59 (6), 965-979 (2005)
16307369
Contact: Alharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alharouf@ars.usda.gov.

FEATURES
source
location/Qualifiers
1..53
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="LCM003 library"
/note="Vector: PCR4 TOPO; cDNA clones from mRNA extracted
from syncytium of soybean roots cv. Kent after infection
by SCN race 3."

ORIGIN
Query Match 62.1%; Score 11.8; DB 8; Length 53;
Best Local Similarity 81.2%; Pred. No. 2.7e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGCTATCTCTTCTT 16
Db 7 CGCAGCAGNATCTCTCC 22

RESULT 31
CB006039/C 55 bp mRNA linear EST 10-JAN-2003
LOCUS VWC028H12_138248 An expressed sequence tag database for abiotic
DEFINITION stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
cDNA clone VWC028H12 5, mRNA sequence.
ACCESSION CB006039
VERSION
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; Vitaceae; Vitis.
1 (bases 1 to 55)
Cushman,J.C.
An expressed sequence tag database for abiotic stressed berries of
Vitis vinifera var. Chardonnay
Unpublished (2002)
Contact: Cushman JC
Department of Biochemistry

```

```

University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 028 row: H column: 12
Seq primer: T3 20mer
High quality sequence stop: 55.
Location/Qualifiers
1..55
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VWC028H12"
/tissue_type="berries"
/dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/clone_lib="An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay"
/note="Vector: lambda Uni-zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

ORIGIN
Query Match 62.1%; Score 11.8; DB 4; Length 55;
Best Local Similarity 86.7%; Pred. No. 2.7e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGGTATCTCTTCTT 17
Db 38 CACGGTATCTCTTCC 24

RESULT 32
AZ459394 62 bp DNA linear GSS 04-OCT-2000
LOCUS AZ459394
DEFINITION 1M0264N10P Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUCG1M0264N10 F, genomic survey sequence.
ACCESSION AZ459394
VERSION
KEYWORDS AZ459394.1 GI:10617519
GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 62)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: N column: 10
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 62.
Location/Qualifiers
1..62
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

```

/db_xref="taxon:10090"
/clone="UUGC1M0264N1.0"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G114732114[gb]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 62;
Best Local Similarity 86.7%; Pred. No. 2.7e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CACGATCTCTCTC 17
42 CACGATCTCTCTC 56

RESULT 33
AA453052/c
LOCUS
DEFINITION
AA453052 63 bp mRNA linear EST 05-JUN-1997
z36f11.r1 Soares total_fetus_Nb2Hr8_9w Homo sapiens cDNA clone
IMAGE:788589 5' similar to TR:G1127764 G1127764 FAF1.; mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AA453052.1 GI:2166721
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 63)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Scheinberg, K., Stepcevic, M., Tan, F., Theising, B.,
White, Y., Wyllie, T., Waterston, R. and Wilson, R.
Washu-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL, contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham.

FEATURES

Location/Qualifiers
1..63
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5986206"
/db_xref="taxon:9606"
/clone="IMAGE:788589"
/dev_stage="8-9 weeks"

/lab_host="DH10B"
/clone_1lb="Soares total_fetus_Nb2Hr8_9w"
/note="Vector: p773D-PacI; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was prepared from mRNA obtained from
pooled 8-9 week (total) fetus material with a Not I -
oligo(dT) primer [5].
TGTTACCAATCTGAGCGGAGCGGCGCTTATTTTTTTTTTTT 3').
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Patricia Bonaldo."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 63;
Best Local Similarity 86.7%; Pred. No. 2.7e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGGATCTCTCTCA 18
47 AAGGATCTCTCTCA 33

RESULT 34
CD533428/c
LOCUS
DEFINITION
CD533428 63 bp mRNA linear EST 31-DEC-2003
31M20 Arabidopsis leaf Senescence Library Arabidopsis thaliana cDNA
3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CD533428.1 GI:40453440
EST.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 63)
Guo, Y., Cai, Z. and Gan, S.
Transcriptome of Arabidopsis leaf senescence
Plant Cell Environ. 27 (5), 521-549 (2004)
Contact: Sheng Gan
Department of Horticulture
Cornell University
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
Tel: 607 254 5418
Fax: 607 255 0599
Email: sg288@cornell.edu
Insert Length: 63 Std Error: 0.00
Seq primer: T7
POLYA=No.

FEATURES

Location/Qualifiers
1..63
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecot_type="Landsberg erecta"
/db_xref="taxon:3702"
/feature_type="Leaf"
/dev_stage="Yellow leaf with Greenish Base Area"
/lab_host="E. coli"
/clone_1lb="Arabidopsis leaf Senescence Library"
/note="Organ: Rosette leaf; Vector: pBluescript SKII+;
Site_1: EcoRI; Site_2: EcoRI; Senescent rosette leaves #5
and #6 (counted from the bottom) were harvested and
immediately frozen in liquid N2. The leaves were visibly
yellow excepted for the leaf base areas that were still
greenish."

ORIGIN

Query Match 62.1%; Score 11.8; DB 5; Length 63;
Best Local Similarity 86.7%; Pred. No. 2.7e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGACGATCTCTCT 15

Db 22 CGAGCTGATCTCT 8

RESULT 35
LOCUS CV305631
DEFINITION C164b04.g7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA sequence.
ACCESSION CV305631
VERSION CV305631
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 65)
Dike,S., Ballija,V.S., Nascimento,L.U., Xuan,Z., Ou,J., Zutavern,T., Palmer,L.E., Hannon,G., Zhang,W.Q. and McCombie,W.R.
The mouse genome: Experimental examination of gene predictions and transcriptional start sites
Genome Res. 14 (12), 2424-2429 (2004)
15574821
JOURNAL Contact: Ballija VS
COMMENT McCombie Laboratory
Cold Spring Harbor Laboratory
500 Sunnyside Blvd, Woodbury, NY 11797, USA
Fax: 516 422 4109
Email: ballija@cshl.org.

FEATURES
source
1..65
/location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_lib="Mouse 5' RACE clones"
/note="Vector: PCR-TOP02.1; Cloned 5' RACE fragments amplified from 5' RACE cDNA generated from 15 pooled mouse tissues and stages: 7, 11, 15, & 17-day total embryo, whole brain, eye, kidney, liver, lung, prostate, submaxillary gland, smooth muscle, spleen, testes and uterus."

ORIGIN
Query Match 62.1%; Score 11.8; DB 8; Length 65;
Best Local Similarity 86.7%; Pred. No. 2.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCACGGTATCTCTT 16
|||||
28 GCAGGCTATCTCTT 42

Db 28 GCAGGCTATCTCTT 42

RESULT 36
PRO053439/c
LOCUS FR0053439 65 bp DNA linear GSS 31-JUL-2002
DEFINITION Fugu rubripes GSS sequence, clone B214J13dH1, genomic survey sequence.
ACCESSION AL689718
VERSION AL689718.1 GI:22079147
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes (Fugu rubripes)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Takifugu.
1 (bases 1 to 65)
Smith,S.F.
Direct Submission
Submitted (08-MAR-2002) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. UK Email: bioc@hgm.mrc.ac.uk

COMMENT Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
DESCR: One pass dye-terminator sequencing of BAC (pBelobAC11) cloned genomic sequence
The BACs can be obtained from www.hgmp.mrc.ac.uk.
location/Qualifiers
1..65
/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="B214J13dH1"
/clone_lib="BAC B214J13"

ORIGIN
Query Match 62.1%; Score 11.8; DB 14; Length 65;
Best Local Similarity 86.7%; Pred. No. 2.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGTATCTCTTCAC 19
|||||
Db 65 CGGTATCTCTTCAC 51

RESULT 37
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LOCUS BH811036
DEFINITION SALK_057115 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_057115, genomic survey sequence.
ACCESSION BH811036
VERSION BH811036.1 GI:20388854
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 66)
Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgil,N.C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
location/Qualifiers
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/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_057115"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="RAC was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN
Query Match 62.1%; Score 11.8; DB 11; Length 66;
Best Local Similarity 86.7%; Pred. No. 2.8e+05;

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LOCUS									
DEFINITION	BH811037		66 bp	DNA	linear	GSS 02-MAY-2002			
ACCESSION	SALK_057118	Arabidopsis thaliana	TDNA insertion lines	Arabidopsis thaliana	genomic clone SALK_057118	genomic survey sequence.			
VERSION	BH811037								
KEYWORDS	BH811037.1	GI:20388885							
SOURCE									
ORGANISM	Arabidopsis thaliana	(thale cress)							
REFERENCE	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.								
AUTHORS	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome								
TITLE	Unpublished (2001)								
JOURNAL	Contact: Joseph R. Ecker								
COMMENT	Salk Institute Genomic Analysis Laboratory (SIGAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu This is single pass sequence recovered from the left border of TDNA. Class: TDNA tagged. Location/Qualifiers								
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	/clone="SALK_057118"								
	/clone_11b="Arabidopsis thaliana TDNA insertion lines"								
	/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html "								
ORIGIN									
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Matches	13;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	5	CGGATCTCTTCAC	19						
Db	13	CGATATCTTCTTCAC	27						
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CZ012701/c									
LOCUS									
DEFINITION	BG5524	BayGenomics Gene Trap Library pGTL1xf	Mus musculus	CDNA,	mRNA	66 bp	linear	GSS 05-JAN-2005	
ACCESSION	CZ012701								
VERSION	CZ012701.1	GI:57118300							
KEYWORDS	GSS.								
SOURCE	Mus musculus	(house mouse)							
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								

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REFERENCE      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
AUTHORS        Sciurogathi; Muridae; Muridae; Murinae; Mus.
TITLE          1 (bases 1 to 66)
JOURNAL        BayGenomics.
COMMENT        http://baygenomics.ucsf.edu/
               Unpublished (2001)
               Contact: BayGenomics
               Bay Area Functional Genomics Consortium (BayGenomics)
               Email: info@baygenomics.ucsf.edu
               Sequence tag generated by 5' RAGE of total RNA from gene trap ES
               cell line. ES cell lines harboring insertion mutation of target
               gene are available upon request from BayGenomics. Annotation
               information available from
               http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACTTYPE&
               CELL_LINE&KEY=BG5524
               Class: Gene Trap.

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    /seq="Male"
    /cell_type="Embryonic stem cell"
    /clone_id="BayGenomics Gene Trap Library pGT11xf"
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ORIGIN
Query Match      62.1%; Score 11.8; DB 13; Length 66;
Best Local Similarity 86.7%; Pred. No. 2.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      4  ACGGATCTCTCTTA 18
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Db      31 AAGCATCTCTTCA 17

RESULT 40
CV305709      68 bp      mRNA      linear      EST 23-SEP-2004
LOCUS         CV305709
DEFINITION    CV305709.68 bp      mRNA      linear      EST 23-SEP-2004
               c14t9g04.g7 Mouse 5' RAGE clones Mus musculus CDNA 5', mRNA
               sequence.
ACCESSION     CV305709
VERSION       CV305709.1 GI:52623042
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 68)
Dike,S., Ballja,V.S., Nascimento,L.U., Xuan,Z., Ou,J., Zutavern,T.,
Palmer,L.B., Hannon,G., Zhang,M.Q. and McCombie,W.R.
The mouse genome: Experimental examination of gene predictions and
transcriptional start sites
Genome Res. 14 (12), 2424-2429 (2004)
15574821
JOURNAL       McCombie Laboratory
PUBMED        Cold Spring Harbor Laboratory
COMMENT        500 Sunnyside Blvd, Woodbury, NY 11797, USA
               Fax: 516 422 4109
               Email: ballja@cshl.org
               Location/Qualifiers
               1..68
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               /mol_type="mRNA"
               /db_xref="taxon:10090"
               /clone_lib="Mouse 5' RAGE clones"
               /note="Vector: PCR-WOP02.1; Cloned 5' RAGE fragments
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               tissues and stages: 7, 11, 15, & 17-day total embryo,
               whole brain, eye, kidney, liver, lung, prostate,

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submaxillary gland, smooth muscle, spleen, testes and
uterus."

Query Match 62.1%; Score 11.8; DB 8; Length 68;
Best Local Similarity 86.7%; Pred. No. 2.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCACGGTATCTCCTT 16
Db 28 GCATGGTATCTCCTT 42

Search completed: August 10, 2006, 08:47:18
Job time : 1827.33 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model1

Run on: August 10, 2006, 07:16:15 ; Search time 69.6667 Seconds
(without alignments)
510.302 Million cell updates/sec

Title: US-10-636-065-29

Perfect score: 19

Sequence: 1 cgcacgctaccccttcac 19

Scoring table: IDENTITY NUC

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1503076

Minimum DB seq length: 0

Maximum DB seq length: 70

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	18	94.7	23	US-09-392-580-3	Sequence 3, Appl
3	15.4	81.1	54	US-09-121-211-5	Sequence 5, Appl
4	13.8	72.6	59	US-08-956-171E-2496	Sequence 2496, Ap
5	13.8	72.6	59	US-08-781-986A-2496	Sequence 2496, Ap
6	13.4	70.5	37	US-08-245-754A-15	Sequence 15, Appl
7	13.4	70.5	37	US-08-587-731-15	Sequence 15, Appl
8	13.2	69.5	20	US-09-198-452A-2460	Sequence 2460, Ap
9	13.2	69.5	29	US-10-345-599B-9	Sequence 9, Appl
10	13.2	69.5	56	US-09-270-767-11190	Sequence 31190, A
11	12.8	67.4	22	US-09-485-529-27	Sequence 27, Appl
12	12.8	67.4	23	US-09-485-529-29	Sequence 29, Appl
13	12.8	67.4	52	US-09-756-301B-26	Sequence 26, Appl
14	12.8	67.4	70	US-08-392-771-2	Sequence 2, Appl
15	12.6	66.3	39	US-09-108-006C-33	Sequence 33, Appl
16	12.6	66.3	50	US-10-131-827-2096	Sequence 2096, Ap
17	12.6	66.3	50	US-10-131-831-2096	Sequence 2096, Ap
18	12.4	65.3	21	US-09-432-978-8933	Sequence 8933, Ap
19	12.4	65.3	29	US-10-007-010-6	Sequence 6, Appl
20	12.4	65.3	35	US-09-485-529-25	Sequence 25, Appl
21	12.4	65.3	47	US-09-422-978-316	Sequence 316, Appl
22	12.2	64.2	21	US-08-811-682-32	Sequence 32, Appl
23	12.2	64.2	24	US-08-697-610-4	Sequence 4, Appl

24	12.2	64.2	24	US-08-349-357-4	Sequence 4, Appl
25	12.2	64.2	25	US-09-396-196G-18978	Sequence 18978, A
26	12.2	64.2	25	US-09-396-196G-77184	Sequence 77184, A
27	12.2	64.2	25	US-09-396-196G-77195	Sequence 77195, A
28	12.2	64.2	50	US-10-131-827-840	Sequence 840, App
29	12.2	64.2	50	US-10-131-831-840	Sequence 840, App
30	12.2	64.2	67	US-09-270-767-27961	Sequence 27961, A
31	12.2	64.2	68	US-08-553-339-1	Sequence 1, Appl
32	12.2	64.2	68	US-09-051-542-1	Sequence 1, Appl
33	12.2	64.2	68	US-08-450-274-1	Sequence 1, Appl
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35	12	63.2	29	US-09-470-276-7	Sequence 7, Appl
36	12	63.2	41	US-08-813-507-46	Sequence 46, Appl
37	12	63.2	41	US-09-464-453-46	Sequence 46, Appl
38	12	63.2	53	US-09-695-437A-48	Sequence 48, Appl
39	11.8	62.1	16	US-09-137-822A-3	Sequence 3, Appl
40	11.8	62.1	20	US-09-917-963-122	Sequence 122, App
41	11.8	62.1	25	US-09-396-196G-49834	Sequence 49834, A
42	11.8	62.1	26	US-09-156-425-3	Sequence 3, Appl
43	11.8	62.1	26	US-08-643-704A-40	Sequence 40, Appl
44	11.8	62.1	27	US-09-253-396A-103	Sequence 103, App
45	11.8	62.1	27	US-09-555-166-47	Sequence 47, Appl
46	11.8	62.1	31	US-08-445-463B-48	Sequence 48, Appl
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48	11.8	62.1	31	US-08-044-857D-48	Sequence 48, Appl
49	11.8	62.1	31	PCT-US94-03437-48	Sequence 48, Appl
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52	11.6	61.1	22	US-08-990-571-54	Sequence 54, Appl
53	11.6	61.1	22	US-09-528-784A-54	Sequence 54, Appl
54	11.6	61.1	22	US-09-569-098B-54	Sequence 54, Appl
55	11.6	61.1	25	US-08-775-164-19	Sequence 19, Appl
56	11.6	61.1	25	US-08-775-609-19	Sequence 19, Appl
57	11.6	61.1	25	US-08-775-607-19	Sequence 19, Appl
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61	11.6	61.1	25	US-09-396-196G-75110	Sequence 75110, A
62	11.6	61.1	25	US-09-396-196G-87092	Sequence 87092, A
63	11.6	61.1	25	PCT-US93-06828-19	Sequence 19, Appl
64	11.6	61.1	26	US-09-550-605B-2	Sequence 2, Appl
65	11.6	61.1	26	US-09-550-605B-5	Sequence 5, Appl
66	11.6	61.1	27	US-08-926-842B-39	Sequence 39, Appl
67	11.6	61.1	27	US-09-818-780-11	Sequence 11, Appl
68	11.6	61.1	27	US-08-926-842B-39	Sequence 39, Appl
69	11.6	61.1	29	US-09-807-897-20	Sequence 20, Appl
70	11.6	61.1	46	US-09-354-664-7	Sequence 7, Appl
71	11.6	61.1	50	US-10-131-827-2429	Sequence 2429, Ap
72	11.6	61.1	50	US-10-131-831-2429	Sequence 2429, Ap
73	11.6	61.1	52	US-08-447-173A-56	Sequence 56, Appl
74	11.4	60.0	20	US-08-466-265-15	Sequence 15, Appl
75	11.4	60.0	25	US-09-396-196G-99034	Sequence 99034, A
76	11.4	60.0	25	US-09-396-196G-99050	Sequence 99050, A
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78	11.4	60.0	25	US-09-396-196G-103409	Sequence 103409, A
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80	11.4	60.0	27	US-08-324-709-10	Sequence 10, Appl
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82	11.4	60.0	27	US-09-133-119-10	Sequence 10, Appl
83	11.4	60.0	27	US-08-192-093A-10	Sequence 10, Appl
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91	11.4	60.0	30	US-08-194-088B-11	Sequence 11, Appl
92	11.4	60.0	30	US-08-435-501-10	Sequence 10, Appl
93	11.4	60.0	30	US-08-435-764-10	Sequence 10, Appl
94	11.4	60.0	30	US-08-792-078-10	Sequence 10, Appl
95	11.4	60.0	30	US-08-194-087-11	Sequence 11, Appl
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97 11.4 60.0 30 7 PCT-US93-04648-11
98 11.4 60.0 30 7 PCT-US93-04717-10
99 11.4 60.0 37 2 US-08-264-115-5
100 11.4 60.0 39 10 5256648-37

Sequence 11, Appl
Sequence 10, Appl
Sequence 5, Appl
Patent No. 5256648

ALIGNMENTS

RESULT 1

US-09-672-717-29
; Sequence 29, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens
US-09-672-717-29

Query Match 100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCTCTTCAC 19
DB 1 CGCAGGTATCTCTCTTCAC 19

RESULT 2

US-09-392-580-3
; Sequence 3, Application US/09392580
; Patent No. 6067173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
; FILE REFERENCE: RTS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-392-580-3

Query Match 94.7%; Score 18; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCACGATATCTCTCTTCAC 19
DB 1 GCACGATATCTCTCTTCAC 18

RESULT 3

US-09-121-211-5/c
; Sequence 5, Application US/09121211
; Patent No. 6750052
; GENERAL INFORMATION:
; APPLICANT: Shinohara, Toshimichi
; APPLICANT: Shingh, Dharendra P.
; APPLICANT: Chylack, Leo T.
; TITLE OF INVENTION: Lens Epithelial Cell Derived Growth
; FILE REFERENCE: B0801/7116
; CURRENT APPLICATION NUMBER: US/09/121,211
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: U.S. 60/053,549
; EARLIER FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: CDS
; LOCATION: (1)...(54)
US-09-121-211-5

Query Match 81.1%; Score 15.4; DB 3; Length 54;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGATATCTCTCTTCAC 19
DB 48 CACGGATATCTCTCTTCAC 32

RESULT 4

US-08-956-171E-2496
; Sequence 2496, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; APPLICANT: Gil H. Choi
; APPLICANT: Patrick S. Dillon
; APPLICANT: Craig A. Rosen
; APPLICANT: Steven C. Barash
; APPLICANT: Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2496:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2496:
US-08-956-171E-2496

Query Match 72.6%; Score 13.8; DB 3; Length 59;
Best Local Similarity 88.2%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTC 17
Db 14 CGCAGGAMTTCTTC 30

RESULT 5

US-08-781-986A-2496
Sequence 2496, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2496:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-2496

Query Match 72.6%; Score 13.8; DB 3; Length 59;
Best Local Similarity 88.2%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTC 17
Db 14 CGCAGGAMTTCTTC 30

RESULT 6

US-08-245-754A-15
Sequence 15, Application US/08245754A
Patent No. 5541110
GENERAL INFORMATION:
APPLICANT: Siegall, Clay B.
TITLE OF INVENTION: Cloning and Expression of a Gene
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/245,754A

FILING DATE: 06-MAY-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Poor, Brian W.

REGISTRATION NUMBER: 32,928

REFERENCE/DOCKET NUMBER: ON0124

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 728-4800

TELEFAX: (206) 727-3601

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-245-754A-15

Query Match 70.5%; Score 13.4; DB 2; Length 37;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAGGTATCTCCTTC 17
Db 1 CAGGTATCTCCTTC 15

RESULT 7

US-08-597-731-15
Sequence 15, Application US/08597731
Patent No. 5932447
GENERAL INFORMATION:
APPLICANT: Siegall, Clay B.
TITLE OF INVENTION: Cloning and Expression of a Gene
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,731
FILING DATE: 07-FEB-1996

```
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,754
; FILING DATE: 06-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 728-4800
; TELEFAX: (206) 727-3601
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-597-731-15
```

Query Match 70.5%; Score 13.4; DB 2; Length 37;

Best Local Similarity 93.3%; Pred. No. 1.5e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 3 GCACGATCTCTCTTC 17
    |||||
Db 1 CATGATCTCTCTTC 15
```

RESULT 8
US-09-198-452A-2460/C
Sequence 2460, Application US/09198452A
Patent No. 6559294

```
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2460
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-2460
```

Query Match 69.5%; Score 13.2; DB 3; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.8e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 2 GCACGATCTCTCTTC 19
    |||||
Db 18 GGACGATCTCTCTTC 1
```

RESULT 9
US-10-345-599B-9
Sequence 9, Application US/10345599B
Patent No. 6946294

```
; GENERAL INFORMATION:
; APPLICANT: KANG, JCONG-GU
; TITLE OF INVENTION: TRANSGENIC PLANT TRANSFORMED WITH A TRANSLATIONALLY
; TITLE OF INVENTION: CONTROLLED TUMOR PROTEIN (TCTP) GENE
; FILE REFERENCE: 4469-114.1US
; CURRENT APPLICATION NUMBER: US/10/345,599B
; CURRENT FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 9
; LENGTH: 29
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; US-10-345-599B-9
```

Query Match 69.5%; Score 13.2; DB 3; Length 29;

Best Local Similarity 83.3%; Pred. No. 1.9e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 CGCAGGATCTCTCTTCA 18
    |||||
Db 9 CGCAGGATCTCTCTTCA 26
```

RESULT 10
US-09-270-767-31190
Sequence 31190, Application US/09270767
Patent No. 6703491

```
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 31190
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-31190
```

Query Match 69.5%; Score 13.2; DB 3; Length 56;

Best Local Similarity 83.3%; Pred. No. 2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 CGCAGGATCTCTCTTCA 18
    |||||
Db 4 CGCAGGATCTCTCTTCA 21
```

RESULT 11
US-09-485-529-27/C
Sequence 27, Application US/09485529
Patent No. 6762348

```
; GENERAL INFORMATION:
; APPLICANT: Harberd, Nicholas P
; APPLICANT: Richards, Donald E
; APPLICANT: Peng, Jinyong
; TITLE OF INVENTION: Genetic Control of Plant Growth and Development
; FILE REFERENCE: 620-91
; CURRENT APPLICATION NUMBER: US/09/485,529
; CURRENT FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/GB98/02383
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: GB 9717192.0
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-485-529-27
```

Query Match 67.4%; Score 12.8; DB 3; Length 22;

Best Local Similarity 87.5%; Pred. No. 2.9e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 4 ACGGATCTCTCTTCA 19
```

Db 19 AGCGTATCTCTTAC 4

RESULT 12

US-09-485-529-29
; Sequence 29, Application US/09485529
; Patent No. 6762348
; GENERAL INFORMATION:
; APPLICANT: Harberd, Nicholas P
; APPLICANT: Richards, Donald E
; APPLICANT: Peng, Jinxiong
; TITLE OF INVENTION: Genetic Control of Plant Growth and Development
; FILE REFERENCE: 620-91
; CURRENT APPLICATION NUMBER: US/09/485,529
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/GB98/02383
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: GB 9717192.0
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-485-529-29

Query Match 67.4%; Score 12.8; DB 3; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.9e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACAGTATCTCTTAC 19
Db 4 AGCGTATCTCTTAC 19

RESULT 13
US-09-756-301B-26/c
; Sequence 26, Application US/09756301B
; Patent No. 6790444
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilecek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-008
; CURRENT APPLICATION NUMBER: US/09/756,301B
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11

; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26

; LENGTH: 52
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial sequence of pLC871

US-09-756-301B-26

Query Match 67.4%; Score 12.8; DB 3; Length 52;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CACGATATCTCTTCA 18
Db 27 CCGATATCTCTTCA 12

RESULT 14

US-08-392-771-2/c
; Sequence 2, Application US/08392771
; Patent No. 5917122
; GENERAL INFORMATION:
; APPLICANT: Byrnie, Guenard
; TITLE OF INVENTION: TETRACYCLINE REPRESSOR-MEDIATED BINARY
; TITLE OF INVENTION: REGULATION SYSTEM FOR CONTROL OF GENE EXPRESSION IN
; TITLE OF INVENTION: TRANSGENIC ANIMALS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAXTER INTERNATIONAL INC.
; ADDRESSEE: LAW DEPARTMENT, MPR-A2S
; STREET: 1620 N. MAWEGAN ROAD
; CITY: MCGRAW PARK
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60085

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/392,771

FILING DATE: 24-FEB-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: MATTEWSON, CHARLES R.

REGISTRATION NUMBER: 30,660

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-473-6693

TELEFAX: 847-473-6933

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 70 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

US-08-392-771-2

Query Match 67.4%; Score 12.8; DB 2; Length 70;
Best Local Similarity 87.5%; Pred. No. 3.3e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACAGTATCTCTTAC 19
Db 63 ACAGTATCTCTTAC 48

```
RESULT 15
US-09-108-006C-33/c
; Sequence 33, Application US/09108006C
; Patent No. 6524613
; GENERAL INFORMATION:
; APPLICANT: Steer, Clifford J.
; Kren, Betsy T.
; Bandyopadhyay, Paramita
; Roy-Chowdhury, Jayanta
; TITLE OF INVENTION: Hepatocellular Chimeraplasty
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kimeragen, Inc.
; STREET: 300 Pleasant Run
; CITY: Newtown
; STATE: PA
; COUNTRY: USA
; ZIP: 18940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,006C
; FILING DATE: 30-Jun-1992
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,288
; FILING DATE: 30-APR-1997
; APPLICATION NUMBER: 60/054,837
; FILING DATE: 05-AUG-1997
; APPLICATION NUMBER: 60/064,996
; FILING DATE: 10-NOV-1997
; APPLICATION NUMBER: 60/074,497
; FILING DATE: 12-FEB-1998
; APPLICATION NUMBER: PCT US 98/08834
; FILING DATE: 30-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebebel, Thomas
; REGISTRATION NUMBER: 29258
; REFERENCE/DOCKET NUMBER: 7991-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-504-4444
; TELEFAX: 215-504-4545
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-108-006C-33

Query Match      66.3%; Score 12.6; DB 3; Length 39;
Best Local Similarity 78.9%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CGCAGCGTATCTCTCTTCAC 19
Db      29 CCCCACATATCTCTCTTCAC 11

RESULT 16
US-10-131-827-2096/c
; Sequence 2096, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; Fry, Kirk
; APPLICANT: Woodward, Robert
```

```
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2096
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2096

Query Match      66.3%; Score 12.6; DB 3; Length 50;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CGCAGCGTATCTCTCTTCAC 19
Db      49 CTCACGTCTCTCTCTGCAC 31

RESULT 17
US-10-131-831-2096/c
; Sequence 2096, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; DISEASES
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2096
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-2096

Query Match      66.3%; Score 12.6; DB 5; Length 50;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CGCAGCGTATCTCTCTTCAC 19
Db      49 CTCACGTCTCTCTCTGCAC 31

RESULT 18
US-09-422-978-8933
; Sequence 8933, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marla
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Ballelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
```

CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8933
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-20198 for SEQ 1068, in complement
US-09-422-978-8933

Query Match 65.3%; Score 12.4; DB 3; Length 21;
Best Local Similarity 92.9%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ACGGATCTCCTTC 17
Db 7 ACTGATCTCCTTC 20

RESULT 19
US-10-007-010-6/c
; Sequence 6, Application US/10007010
; Patent No. 6828151
; GENERAL INFORMATION:
; APPLICANT: Alexander H. Borchers
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
; FILE REFERENCE: RTS-0345
; CURRENT APPLICATION NUMBER: US/10/007,010
; CURRENT FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-007-010-6

Query Match 65.3%; Score 12.4; DB 3; Length 29;
Best Local Similarity 92.9%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGATCTCCTT 16
Db 20 CACGGATCTCCTT 7

RESULT 20
US-09-485-529-25
; Sequence 25, Application US/09485529
; Patent No. 6762348
; GENERAL INFORMATION:
; APPLICANT: Harberd, Nicholas P
; APPLICANT: Richards, Donald E
; APPLICANT: Peng, Jinyong
; TITLE OF INVENTION: Genetic Control of Plant Growth and Development
; FILE REFERENCE: 620-91
; CURRENT APPLICATION NUMBER: US/09/485,529
; CURRENT FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/GB98/02383
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: GB 9717192.0
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 108

SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-485-529-25

Query Match 65.3%; Score 12.4; DB 3; Length 35;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGTATCTCTTCAC 19
Db 1 GGTATCTCTTCAC 14

RESULT 21
US-09-422-978-316/c
; Sequence 316, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 316
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-14179-191 : polymorphic base A or G
US-09-422-978-316

Query Match 65.3%; Score 12.4; DB 3; Length 47;
Best Local Similarity 81.2%; Pred. No. 5.1e+03;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGGATCTCCTTCAC 19
Db 39 ACGGATCTCCTTCAY 24

RESULT 22
US-08-811-682-32/c
; Sequence 32, Application US/08811682
; Patent No. 6331616
; GENERAL INFORMATION:
; APPLICANT: Tompkins, Wayne A.F.
; APPLICANT: Tompkins, Mary B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Feline Immunodeficiency Virus Clone
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Bell Seitzer Park & Gibson
; STREET: PO Drawer 34009
; CITY: Charlotte
; STATE: No. 6331616th Carolina
; COUNTRY: USA
; ZIP: 28234

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,662
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 5051-332
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-811-682-32
```

```
Query Match
Best Local Similarity 64.2%; Score 12.2; DB 3; Length 21;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 GCACGGTATCTCCTTCA 18
DB 18 GCACGATATCTCCTTA 2
```

RESULT 23

```
US-08-697-610-4
Sequence 4, Application US/08697610
Patent No. 6172187
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaki
TITLE OF INVENTION: CD40 Associated Proteins
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,610
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/349,357
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1203
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
```

```
STRANDEDNESS: single
TOPOLOGY: linear
US-08-697-610-4
```

```
Query Match
Best Local Similarity 64.2%; Score 12.2; DB 3; Length 24;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 3 CACGGTATCTCCTGCAC 19
DB 8 CACTGTCTCTCTGCAC 24
```

RESULT 24

```
US-08-349-357-4
Sequence 4, Application US/08349357
Patent No. 6265556
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaki
TITLE OF INVENTION: CD40 Associated Proteins
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/349,357
FILING DATE: 02-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1203
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-349-357-4
```

Query Match

```
Best Local Similarity 64.2%; Score 12.2; DB 3; Length 24;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 CACGGTATCTCCTGCAC 19
DB 8 CACTGTCTCTCTGCAC 24
```

RESULT 25

```
US-09-396-18978
Sequence 18978, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mitmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
```

;; CURRENT APPLICATION NUMBER: US/09/396,196G
;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 18978
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-09-396-196G-18978

Query Match 64.2%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CACGGTATCTCTTCAC 19
Db 7 CACGGCATCTACTCCAC 23

RESULT 26
US-09-396-196G-77184
;; Sequence 77184, Application US/09396196G
;; Patent No. 6821724
;; GENERAL INFORMATION:
;; APPLICANT: Michael Miltmann
;; APPLICANT: David Lockhart
;; APPLICANT: Affymetrix, Inc.
;; TITLE OF INVENTION: Methods of Genetic Analysis
;; FILE REFERENCE: 3101.1
;; CURRENT APPLICATION NUMBER: US/09/396,196G
;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 77184
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-09-396-196G-77184

Query Match 64.2%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCTTC 17
Db 9 CGCAGTATCTACTTTC 25

RESULT 27
US-09-396-196G-77195
;; Sequence 77195, Application US/09396196G
;; Patent No. 6821724
;; GENERAL INFORMATION:
;; APPLICANT: Michael Miltmann
;; APPLICANT: David Mack
;; APPLICANT: David Lockhart
;; APPLICANT: Affymetrix, Inc.
;; TITLE OF INVENTION: Methods of Genetic Analysis
;; FILE REFERENCE: 3101.1
;; CURRENT APPLICATION NUMBER: US/09/396,196G
;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 77195
;; LENGTH: 25
;; TYPE: DNA

;; ORGANISM: Mus musculus
US-09-396-196G-77195

Query Match 64.2%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCTTC 17
Db 3 CGCAGTATCTACTTTC 19

RESULT 28
US-10-131-827-840
;; Sequence 840, Application US/10131827
;; Patent No. 6905827
;; GENERAL INFORMATION:
;; APPLICANT: Wohlgenuth, Jay
;; APPLICANT: Fry, Kirk
;; APPLICANT: Woodward, Robert
;; APPLICANT: Ly, Ngoc
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
;; FILE REFERENCE: 506612000120
;; CURRENT APPLICATION NUMBER: US/10/131,827
;; CURRENT FILING DATE: 2002-09-06
;; PRIOR APPLICATION NUMBER: US 10/006,290
;; PRIOR FILING DATE: 2001-10-22
;; PRIOR APPLICATION NUMBER: US 60/296,764
;; PRIOR FILING DATE: 2001-06-08
;; NUMBER OF SEQ ID NOS: 9090
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 840
;; LENGTH: 50
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-131-827-840

Query Match 64.2%; Score 12.2; DB 3; Length 50;
Best Local Similarity 82.4%; Pred. No. 6.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCTTCA 18
Db 26 GCCCGGTACGTCTTCA 42

RESULT 29
US-10-131-831-840
;; Sequence 840, Application US/10131831
;; Patent No. 7026121
;; GENERAL INFORMATION:
;; APPLICANT: Wohlgenuth, Jay
;; APPLICANT: Fry, Kirk
;; APPLICANT: Woodward, Robert
;; APPLICANT: Ly, Ngoc
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
;; FILE REFERENCE: 506612000121
;; CURRENT APPLICATION NUMBER: US/10/131,831
;; CURRENT FILING DATE: 2002-08-05
;; PRIOR APPLICATION NUMBER: US 10/006,290
;; PRIOR FILING DATE: 2001-10-22
;; PRIOR APPLICATION NUMBER: US 60/296,764
;; PRIOR FILING DATE: 2001-06-08
;; NUMBER OF SEQ ID NOS: 9190
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 840
;; LENGTH: 50
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-131-831-840

Query Match 64.2%; Score 12.2; DB 5; Length 50;
Best Local Similarity 82.4%; Pred. No. 6.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTTCA 18
Db 26 GCCCGGTAGCTCCTTCA 42

RESULT 30

US-09-270-767-27961/C
; Sequence 27961, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 1999-03-17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27961
; LENGTH: 67
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-27961

Query Match 64.2%; Score 12.2; DB 3; Length 67;
Best Local Similarity 82.4%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTC 17
Db 58 CGCAGGTATCTCCTTC 42

RESULT 31

US-08-553-339-1
; Sequence 1, Application US/08553339A
; Patent No. 5856300
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W
; APPLICANT: Carol, Toch A
; TITLE OF INVENTION: COMPOSITIONS COMPRISING COMPLEMENT RELATED PROTEINS AND
; TITLE OF INVENTION: CARBOHYDRATES, AND METHODS FOR PRODUCING AND USING
; FILE REFERENCE: TCS-409, 1P US sequence list
; CURRENT APPLICATION NUMBER: US/08/553,339A
; EARLIER FILING DATE: 1995-11-13
; EARLIER APPLICATION NUMBER: US 08/061,982
; EARLIER FILING DATE: 1993-05-17
; EARLIER APPLICATION NUMBER: PCT/US94/05285
; EARLIER FILING DATE: 1994-05-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: commercial
US-08-553-339-1

Query Match 64.2%; Score 12.2; DB 2; Length 68;
Best Local Similarity 82.4%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTC 17
Db 1 CGCCGGTCTCCCTTC 17

RESULT 32
US-09-061-542-1
; Sequence 1, Application US/09061542
; Patent No. 5976540
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W
; APPLICANT: Carol, Toch A
; TITLE OF INVENTION: COMPOSITIONS COMPRISING COMPLEMENT RELATED PROTEINS AND
; TITLE OF INVENTION: CARBOHYDRATES, AND METHODS FOR PRODUCING AND USING
; FILE REFERENCE: TCS-409, 1P US-2 sequence list
; CURRENT APPLICATION NUMBER: US/09/061,542
; EARLIER FILING DATE: 1998-04-16
; EARLIER APPLICATION NUMBER: US 08/553,339
; EARLIER FILING DATE: 1995-11-13
; EARLIER APPLICATION NUMBER: US 08/061,982
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: commercial
US-09-061-542-1

Query Match 64.2%; Score 12.2; DB 2; Length 68;
Best Local Similarity 82.4%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTC 17
Db 1 CGCCGGTCTCCCTTC 17

RESULT 33

US-08-450-274-1
; Sequence 1, Application US/08450274
; Patent No. 6193979
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Toch, Carol A.
; TITLE OF INVENTION: Compositions comprising complement
; TITLE OF INVENTION: related proteins and carbohydrates and methods for producing ar
; TITLE OF INVENTION: using said compositions
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,274
; FILING DATE: (concurrently herewith)
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; FILING DATE: 12-May-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS-101-PCON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-450-274-1

Query Match 64.2%; Score 12.2; DB 3; Length 68;
Best Local Similarity 82.4%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CGCAGGATCTCTCCTTC 17
1 CGCCCGGCTCTCCCTTC 17

RESULT 34
PCT-US94-05285A-1
Sequence 1, Application PC/TUS9405285A
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
APPLICANT: Roth, Carol A.
TITLE OF INVENTION: Compositions comprising complement
TITLE OF INVENTION: related proteins and carbohydrates, and methods for producing
TITLE OF INVENTION: using said compositions
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: T Cell Sciences, Inc.
STREET: 38 Sidney Street
CITY: Cambridge
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05285A
FILING DATE: 12-MAY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/061,982
FILING DATE: 17-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,269
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-621-1400
TELEFAX: 617-621-0627
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
DESCRIPTION: DNA
PCT-US94-05285A-1

Query Match 64.2%; Score 12.2; DB 7; Length 68;
Best Local Similarity 82.4%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CGCAGGATCTCTCCTTC 17
1 CGCCCGGCTCTCCCTTC 17

RESULT 35
US-09-470-276-7
Sequence 7, Application US/09470276
Patent No. 6670460
GENERAL INFORMATION:
APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.
APPLICANT: KOLODNER, Richard
APPLICANT: WINAND, Nena
TITLE OF INVENTION: A METHOD OF DETECTION OF ALTERATIONS IN MSH5
FILE REFERENCE: 700157/47483C
CURRENT APPLICATION NUMBER: US/09/470,276
CURRENT FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 60/051,686
PRIOR FILING DATE: 1997-07-03
PRIOR APPLICATION NUMBER: PCT/US98/13850
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 29
TYPE: DNA
ORGANISM: Human
US-09-470-276-7

Query Match 63.2%; Score 12; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 GGTATCTCTCCTTC 17
9 GGTATCTCTCCTTC 20

RESULT 36
US-08-813-507-46/c
Sequence 46, Application US/08813507
Patent No. 6114116
GENERAL INFORMATION:
APPLICANT: Lemieux, Bertrand
APPLICANT: Landry, Benoit S.
APPLICANT: Sapolsky, Ronald J.
TITLE OF INVENTION: Brascica Polymorphisms
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,507
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,069
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-030100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 576-0200
TELEFAX: 415 576-0200
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-813-507-46

Query Match 63.2%; Score 12; DB 3; Length 41;
Best Local Similarity 85.7%; Pred. No. 8.2e+03;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCA 18
DB 21 YGGTCTCTCCTTCA 8

RESULT 37
US-09-464-453-46/C
Sequence 46, Application US/09464453
Patent No. 6358686
GENERAL INFORMATION:
APPLICANT: Lemieux, Bertrand
Landry, Benoit S.
Sapoleky, Ronald J.
TITLE OF INVENTION: Brassica Polymorphisms
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/464,453
FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/813,507
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-030100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 576-0200
TELEFAX: 415 576-0200

INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-464-453-46

Query Match 63.2%; Score 12; DB 3; Length 41;
Best Local Similarity 85.7%; Pred. No. 8.2e+03;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCA 18
DB 21 YGGTCTCTCCTTCA 8

RESULT 38
US-09-695-437A-48/C
Sequence 48, Application US/09695437A
Patent No. 6803203

GENERAL INFORMATION:
APPLICANT: Brookhaven Science Associates
APPLICANT: Anderson, Carl W
APPLICANT: Connolly, Margery A
TITLE OF INVENTION: DNA-PK Assay
FILE REFERENCE: BSA 01-02
CURRENT APPLICATION NUMBER: US/09/695,437A
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/398,139
PRIOR FILING DATE: 1995-03-03
PRIOR APPLICATION NUMBER: 08/132,284
PRIOR FILING DATE: 1993-10-06
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH: 53
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sense primer sequence
US-09-695-437A-48

Query Match 63.2%; Score 12; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTATCTCCTTC 17
DB 32 GGTATCTCCTTC 21

RESULT 39
US-09-137-822A-3/C
Sequence 3, Application US/09137822A
Patent No. 6979536
GENERAL INFORMATION:
APPLICANT: NAESBY, MICHAEL
TITLE OF INVENTION: SMALL TRIPLEX FORMING PNA OLIGOS
FILE REFERENCE: 108382-08067
CURRENT APPLICATION NUMBER: US/09/137,822A
CURRENT FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: EP 97 114 512.3
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 3
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-137-822A-3

Query Match 62.1%; Score 11.8; DB 4; Length 16;
Best Local Similarity 86.7%; Pred. No. 9.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCAC 19
DB 16 CGGTATCTTCTGCAC 2

RESULT 40
US-09-917-963-122/C
Sequence 122, Application US/09917963
Patent No. 6767739
GENERAL INFORMATION:
APPLICANT: Rosanne M. Crooke
APPLICANT: Mark J. Graham
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: ISPH-0591

; CURRENT APPLICATION NUMBER: US/09/917,963
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 137
; SEQ ID NO 122
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-917-963-122

Query Match 62.1%; Score 11.8; DB 3; length 20;
Best Local Similarity 86.7%; Pred. No. 9.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGGTATCTCCTTCA 18
||| |||||
Db 15 ACGATGCTCCTTCA 1

Search completed: August 10, 2006, 08:50:50
Job time : 71.6667 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model1

Run on: August 10, 2006, 08:11:42 ; Search time 272.667 Seconds
(without alignments)
485.841 Million cell updates/sec

Title: US-10-636-065-29
Perfect score: 19
Sequence: 1 cgcacgctactctctcac 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 524920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 340112

Minimum DB seq length: 19
Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :
1: N Geneseq_8:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	19	100.0	19	6	ABK93682		ABK93682 Human inh
2	19	100.0	19	14	AEA10008		AEA10008 Antisense
3	19	100.0	19	14	AEA10086		AEA10086 Antisense
4	15	78.9	19	14	ADK86146		ADK86146 XIAP targ
5	15	78.9	19	14	ADK86613		ADK86613 XIAP targ
6	14	73.7	19	10	ADP68184		ADP68184 Human ant
7	14	73.7	19	10	ADP68262		ADP68262 Human ant
8	14	73.7	19	14	AEA10122		AEA10122 Antisense
9	14	73.7	19	14	AEA10076		AEA10076 Antisense
10	14	73.7	19	14	AEA10108		AEA10108 Antisense
11	14	73.7	19	14	AEA09518		AEA09518 Antisense
12	14	73.7	19	14	AEA09518		AEA09518 Antisense
13	14	73.7	19	14	AEA09596		AEA09596 Antisense
14	13	68.4	19	14	AEK33674		AEK33674 Forward p
15	12.6	66.3	19	14	AEA10089		AEA10089 Antisense
16	12.4	65.3	19	12	ADQ61052		ADQ61052 Anti-HCK
17	11.8	62.1	19	2	AAK24944		AAK24944 Mouse oes
18	11.8	62.1	19	2	AAK33389		AAK33389 Murine MB

C	19	11.8	62.1	19	15	AEF14562	AEF14562 Human cho
20	21	11.4	60.0	19	10	ADF73037	ADF73037 DNA seque
21	22	11.4	60.0	19	10	ACD28194	ACD28194 Human rep
22	22	11.1	57.9	19	3	AAZ73203	AAZ73203 Human bla
23	23	11.1	57.9	19	12	ADQ61051	ADQ61051 Anti-HCK
24	24	11.1	57.9	19	14	ADY83894	ADY83894 Escherich
25	25	11.1	57.9	19	14	ADY83902	ADY83902 Escherich
26	26	11.1	57.9	19	14	ABA02570	ABA02570 Cholester
27	27	11.1	57.9	19	14	AEA02470	AEA02470 Cholester
28	28	11.1	57.9	19	14	AEA34343	AEA34343 Human hai
29	29	11.1	57.9	19	14	AEA34343	AEA34343 Human hai
30	30	10.8	56.8	19	3	AAA85544	AAA85544 Cyclin A1
31	31	10.8	56.8	19	3	AAA85544	AAA85544 Cyclin A1
32	32	10.8	56.8	19	3	AAA85542	AAA85542 Cyclin A1
33	33	10.8	56.8	19	3	AAA85543	AAA85543 Cyclin A1
34	34	10.8	56.8	19	3	AAA85448	AAA85448 Cyclin A1
35	35	10.8	56.8	19	3	AAC59851	AAC59851 Oligonuc1
36	36	10.8	56.8	19	5	AAH60704	AAH60704 Cyclin A1
37	37	10.8	56.8	19	5	AAH60705	AAH60705 Cyclin A1
38	38	10.8	56.8	19	5	AAH60706	AAH60706 Cyclin A1
39	39	10.8	56.8	19	5	AAH60610	AAH60610 Cyclin A1
40	40	10.8	56.8	19	5	AAH60707	AAH60707 Cyclin A1
41	41	10.8	56.8	19	11	ADL79714	ADL79714 Human HER
42	42	10.8	56.8	19	11	ADL79407	ADL79407 Human HER
43	43	10.8	56.8	19	12	ADQ61178	ADQ61178 Anti-RYK
44	44	10.8	56.8	19	13	ADK16127	ADK16127 Human DNA
45	45	10.8	56.8	19	14	AEK73574	AEK73574 RNAi sens
46	46	10.8	56.8	19	14	AEK73570	AEK73570 RNAi sens
47	47	10.8	56.8	19	14	AEA67118	AEA67118 Human hai
48	48	10.8	56.8	19	14	AEA67118	AEA67118 Human hai
49	49	10.8	56.8	19	14	AEA67114	AEA67114 Human hai
50	50	10.8	56.8	19	14	AEA67114	AEA67114 Human hai
51	51	10.8	56.8	19	14	AEA67119	AEA67119 Human hai
52	52	10.8	56.8	19	14	AEA67122	AEA67122 Human hai
53	53	10.8	56.8	19	14	AEA67121	AEA67121 Human hai
54	54	10.8	56.8	19	14	AEA6716	AEA6716 Human hai
55	55	10.8	56.8	19	14	AEA6717	AEA6717 Human hai
56	56	10.8	56.8	19	14	AEA6717	AEA6717 Human hai
57	57	10.8	56.8	19	14	AEA6717	AEA6717 Human hai
58	58	10.8	56.8	19	14	AEA67120	AEA67120 Human hai
59	59	10.8	56.8	19	14	AEA6715	AEA6715 Human hai
60	60	10.6	55.8	19	15	ABG07498	ABG07498 Human R58
61	61	10.6	55.8	19	4	AAH39730	AAH39730 SNP spec1
62	62	10.6	55.8	19	4	AAH45386	AAH45386 Corynebact
63	63	10.6	55.8	19	10	ADP54371	ADP54371 Human GAB
64	64	10.6	55.8	19	10	ADP54035	ADP54035 Human GAB
65	65	10.6	55.8	19	10	ACA61058	ACA61058 Giunardi
66	66	10.6	55.8	19	10	ACF42633	ACF42633 Human ALM
67	67	10.6	55.8	19	11	ADM06319	ADM06319 Human PCR
68	68	10.6	55.8	19	12	ADJ37073	ADJ37073 Gene 216
69	69	10.6	55.8	19	12	ADP26972	ADP26972 Human P-c
70	70	10.6	55.8	19	13	ACL75990	ACL75990 SARS coro
71	71	10.6	55.8	19	13	ACL75989	ACL75989 SARS coro
72	72	10.6	55.8	19	13	ACL75279	ACL75279 SARS coro
73	73	10.6	55.8	19	13	ACL76335	ACL76335 SARS coro
74	74	10.6	55.8	19	13	ACL75987	ACL75987 SARS coro
75	75	10.6	55.8	19	13	ACL76642	ACL76642 SARS coro
76	76	10.6	55.8	19	13	ACL79502	ACL79502 SARS coro
77	77	10.6	55.8	19	13	ACL75278	ACL75278 SARS coro
78	78	10.6	55.8	19	13	ACL75277	ACL75277 SARS coro
79	79	10.6	55.8	19	14	ABE05405	ABE05405 Human IL-
80	80	10.6	55.8	19	14	ABE05182	ABE05182 Human IL-
81	81	10.6	55.8	19	14	ABE15019	ABE15019 Human IL-
82	82	10.6	55.8	19	14	ABE15242	ABE15242 Human IL-
83	83	10.6	55.8	19	14	ABE33284	ABE33284 Human GAB
84	84	10.6	55.8	19	14	ABE33284	ABE33284 Human GAB
85	85	10.6	55.8	19	14	ABE20703	ABE20703 Human ALM
86	86	10.6	55.8	19	14	ABE89249	ABE89249 Human CDN
87	87	10.6	55.8	19	14	ABE43437	ABE43437 Human hai
88	88	10.6	55.8	19	14	ABE43436	ABE43436 Human hai
89	89	10.6	55.8	19	14	ABE43438	ABE43438 Human hai
90	90	10.6	55.8	19	14	ABE43435	ABE43435 Human hai
91	91	10.4	54.7	19	3	AAA85546	AAA85546 Cyclin A1

92	10.4	54.7	19	3	AAZ70584	Human b1a	c 165	10	52.6	19	14	ADY87409
93	10.4	54.7	19	3	AAZ71863	Human b1a	c 166	10	52.6	19	14	AEA34632
94	10.4	54.7	19	5	AAH60708	Cyclin A1	c 167	10	52.6	19	14	AEA44556
95	10.4	54.7	19	12	AD51075	Human NOV	c 168	10	52.6	19	14	AED36644
96	10.4	54.7	19	12	ADM86892	Example n	c 169	10	52.6	19	14	AED36217
97	10.4	54.7	19	12	ADQ27225	RNA inter	c 170	10	52.6	19	14	AED64040
98	10.4	54.7	19	14	AEBO5347	Human IL-	c 171	10	52.6	19	14	AEBO3031
99	10.4	54.7	19	14	AEBO5124	Human IL-	c 172	10	52.6	19	14	AEBA4331
100	10.4	54.7	19	14	AEC14961	Human IL-	c 173	10	52.6	19	14	AEBA4332
101	10.4	54.7	19	14	AEC15184	Human IL-	c 174	10	52.6	19	14	AEBA3635
102	10.4	54.7	19	15	AE871863	Human K10	c 175	9.8	51.6	19	2	AAQ91357
103	10.2	53.7	19	2	AAQ06429	Oligonucle	c 176	9.8	51.6	19	2	AAH66907
104	10.2	53.7	19	3	AAA29755	Construct	c 177	9.8	51.6	19	2	AAZ06875
105	10.2	53.7	19	6	ABK41152	Human glia	c 178	9.8	51.6	19	2	AAK61047
106	10.2	53.7	19	10	ADP84170	Human obe	c 179	9.8	51.6	19	2	AAZ01238
107	10.2	53.7	19	10	ADP84170	Human bre	c 180	9.8	51.6	19	3	AAZ73173
108	10.2	53.7	19	10	ADP83907	Human bre	c 181	9.8	51.6	19	3	AAZ73173
109	10.2	53.7	19	11	ADN34338	Lower str	c 182	9.8	51.6	19	4	AAZ01911
110	10.2	53.7	19	11	ADN34099	Upper str	c 183	9.8	51.6	19	4	AAZ01911
111	10.2	53.7	19	12	ADQ61980	Anti-EDG7	c 184	9.8	51.6	19	4	AAH42019
112	10.2	53.7	19	14	ADZ53940	Huntingt	c 185	9.8	51.6	19	4	AAH42018
113	10.2	53.7	19	14	ADZ55692	Huntingt	c 186	9.8	51.6	19	10	ADP36724
114	10.2	53.7	19	14	ADZ53939	Huntingt	c 187	9.8	51.6	19	10	ADP37048
115	10.2	53.7	19	14	ADZ55693	Huntingt	c 188	9.8	51.6	19	10	ADP31507
116	10.2	53.7	19	14	ADZ55690	Huntingt	c 189	9.8	51.6	19	10	ADP31784
117	10.2	53.7	19	14	ADZ53938	Huntingt	c 190	9.8	51.6	19	10	ADP54265
118	10.2	53.7	19	14	ADZ55691	Huntingt	c 191	9.8	51.6	19	10	ADP53929
119	10.2	53.7	19	14	ADZ55694	Huntingt	c 192	9.8	51.6	19	10	ADP54214
120	10.2	53.7	19	14	ADZ53941	Huntingt	c 193	9.8	51.6	19	10	ADP54550
121	10.2	53.7	19	14	ADZ53942	Huntingt	c 194	9.8	51.6	19	11	ADL79673
122	10.2	53.7	19	14	AEA44595	Human TRP	c 195	9.8	51.6	19	11	ADL79366
123	10.2	53.7	19	14	AEA34671	Human TRP	c 196	9.8	51.6	19	12	ADK95375
124	10.2	53.7	19	14	AE829096	Human g1R	c 197	9.8	51.6	19	12	ADQ27824
125	10.2	53.7	19	14	AE854778	Human tarc	c 198	9.8	51.6	19	12	ADQ27826
126	10.2	53.7	19	14	AE826225	Human cyc	c 199	9.8	51.6	19	12	ADY14668
127	10.2	53.7	19	14	AE825986	Human gyc	c 200	9.8	51.6	19	14	ADV94023
128	10.2	53.7	19	14	AE829125	Target/si	c 201	9.8	51.6	19	14	ADV93940
129	10.2	53.7	19	14	AE829381	siRNA low	c 202	9.8	51.6	19	14	ADY50713
130	10.2	53.7	19	14	AE829128	Target/si	c 203	9.8	51.6	19	14	ADY87977
131	10.2	53.7	19	14	AE829377	siRNA low	c 204	9.8	51.6	19	14	ADY88301
132	10.2	53.7	19	14	AE829127	Target/si	c 205	9.8	51.6	19	14	ADZ82509
133	10.2	53.7	19	14	AE829127	Target/si	c 206	9.8	51.6	19	14	ADZ82935
134	10.2	53.7	19	14	AE829129	Target/si	c 207	9.8	51.6	19	14	AEA02625
135	10.2	53.7	19	14	AE829380	siRNA low	c 208	9.8	51.6	19	14	AEA02625
136	10.2	53.7	19	14	AE829126	Target/si	c 209	9.8	51.6	19	14	AEA34532
137	10.2	53.7	19	14	AE829378	siRNA low	c 210	9.8	51.6	19	14	AEA44456
138	10.2	53.7	19	15	AE857146	Human hun	c 211	9.8	51.6	19	14	AEBA6332
139	10.2	53.7	19	15	AE857148	Human hun	c 212	9.8	51.6	19	14	AEBA6409
140	10.2	53.7	19	15	AE858901	Human hun	c 213	9.8	51.6	19	14	AEBA6257
141	10.2	53.7	19	15	AE858902	Human hun	c 214	9.8	51.6	19	14	AEBA6257
142	10.2	53.7	19	15	AE858899	Human hun	c 215	9.8	51.6	19	14	AEBA6257
143	10.2	53.7	19	15	AE857149	Human hun	c 216	9.8	51.6	19	14	AEBA6257
144	10.2	53.7	19	15	AE858898	Human hun	c 217	9.8	51.6	19	14	AEBA6257
145	10.2	53.7	19	15	AE857147	Human hun	c 218	9.8	51.6	19	14	AEBA6257
146	10.2	53.7	19	15	AE857150	Human hun	c 219	9.8	51.6	19	14	AEBA6257
147	10.2	53.7	19	15	AE858900	Human hun	c 220	9.8	51.6	19	14	AEBA6257
148	10.2	53.7	19	15	AE858900	Human hun	c 221	9.8	51.6	19	14	AEBA6257
149	10.2	53.7	19	2	AAH62761	Murine bc	c 222	9.8	51.6	19	14	AEBA6257
150	10.2	53.7	19	2	AAH62761	Primer us	c 223	9.8	51.6	19	14	AEBA6257
151	10.2	53.7	19	3	AAH62761	Primer us	c 224	9.8	51.6	19	14	AEBA6257
152	10.2	53.7	19	3	AAH62761	Primer us	c 225	9.8	51.6	19	14	AEBA6257
153	10.2	53.7	19	3	AAH62761	Primer us	c 226	9.8	51.6	19	14	AEBA6257
154	10.2	53.7	19	8	ACD20499	Human NOV	c 227	9.8	51.6	19	14	AEBA6257
155	10.2	53.7	19	8	ACD20499	Human NOV	c 228	9.8	51.6	19	14	AEBA6257
156	10.2	53.7	19	10	ADP36156	Human VEG	c 229	9.8	51.6	19	14	AEBA6257
157	10.2	53.7	19	10	ADP36156	Human VEG	c 230	9.8	51.6	19	14	AEBA6257
158	10.2	53.7	19	10	ADP36156	Human VEG	c 231	9.8	51.6	19	14	AEBA6257
159	10.2	53.7	19	12	ADP36156	Human VEG	c 232	9.8	51.6	19	14	AEBA6257
160	10.2	53.7	19	12	ADP36156	Human VEG	c 233	9.8	51.6	19	14	AEBA6257
161	10.2	53.7	19	12	ADP36156	Human VEG	c 234	9.8	51.6	19	14	AEBA6257
162	10.2	53.7	19	12	ADP36156	Human VEG	c 235	9.8	51.6	19	14	AEBA6257
163	10.2	53.7	19	14	ADY83910	Becherich	c 236	9.8	51.6	19	14	AEBA6257
164	10.2	53.7	19	14	ADY83910	Becherich	c 237	9.8	51.6	19	14	AEBA6257

C 238	9.8	51.6	19	14	AEBS3631	Aee53631 Human hai	311	9.4	49.5	19	13	ADUS9910	Adus9910 Human pap
C 239	9.8	51.6	19	14	AEBS3630	Aee53630 Human hai	312	9.4	49.5	19	13	ADUS9934	Adus9934 Human pap
C 240	9.8	51.6	19	14	AEBS3635	Aee53635 Human hai	313	9.4	49.5	19	13	ADT26142	Adt26142 Human pap
C 241	9.6	50.5	19	2	AAZ40531	Aaz40531 Human STE	314	9.4	49.5	19	14	ADY94081	Ady94081 Presentill
C 242	9.6	50.5	19	2	AAV72609	Aav72609 Human coa	315	9.4	49.5	19	14	ADY93998	Ady93998 Presentill
C 243	9.6	50.5	19	2	AAK31877	Aak31877 S. aureus	316	9.4	49.5	19	14	ADY03176	Ady03176 Extend pr
C 244	9.6	50.5	19	4	AAZ72756	Aaz72756 Human bla	317	9.4	49.5	19	14	ADY52838	Ady52838 Human CHR
C 245	9.6	50.5	19	4	AAAF82399	Aaf82399 Mealworm	318	9.4	49.5	19	14	ADY52838	Ady52838 Escherich
C 246	9.6	50.5	19	5	ABAB82144	Abab82144 Zmaxi gen	319	9.4	49.5	19	14	ADY83874	Ady83874 Escherich
C 247	9.6	50.5	19	6	ABK41008	Abk41008 Human obe	320	9.4	49.5	19	14	ADY83882	Ady83882 Escherich
C 248	9.6	50.5	19	6	ABQ74049	Abq74049 SSO probe	321	9.4	49.5	19	14	ADY83906	Ady83906 Escherich
C 249	9.6	50.5	19	8	ABK22941	Abk22941 Human hbm	322	9.4	49.5	19	14	ADY83901	Ady83901 Escherich
C 250	9.6	50.5	19	8	ACC45524	Acc45524 Human HBM	323	9.4	49.5	19	14	ADY83892	Ady83892 Escherich
C 251	9.6	50.5	19	10	ADBB98222	Adbb98222 Sequence	324	9.4	49.5	19	14	ADY83893	Ady83893 Escherich
C 252	9.6	50.5	19	10	ADBB98222	Adbb98222 Sequence	325	9.4	49.5	19	14	ADY83900	Ady83900 Escherich
C 253	9.6	50.5	19	10	ADBB98222	Adbb98222 Sequence	326	9.4	49.5	19	14	ADY83903	Ady83903 Escherich
C 254	9.6	50.5	19	10	ADBB98222	Adbb98222 Sequence	327	9.4	49.5	19	14	ADY83895	Ady83895 Escherich
C 255	9.6	50.5	19	10	ADBB98222	Adbb98222 Sequence	328	9.4	49.5	19	14	ADY83895	Ady83895 Escherich
C 256	9.6	50.5	19	11	ADL69874	Adl69874 Human TER	329	9.4	49.5	19	14	ADY87950	Ady87950 VEGFR b1R
C 257	9.6	50.5	19	11	ADL69874	Adl69874 Human TER	330	9.4	49.5	19	14	ADY87950	Ady87950 VEGFR b1R
C 258	9.6	50.5	19	12	ADH68492	Adh68492 Human GIP	331	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 259	9.6	50.5	19	12	ADH68492	Adh68492 Human GIP	332	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 260	9.6	50.5	19	13	ADQ94230	Adq94230 Human HNF	333	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 261	9.6	50.5	19	13	ADQ94230	Adq94230 Human HNF	334	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 262	9.6	50.5	19	13	ADQ94230	Adq94230 Human HNF	335	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 263	9.6	50.5	19	13	ADQ94230	Adq94230 Human HNF	336	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 264	9.6	50.5	19	13	ADQ94230	Adq94230 Human HNF	337	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 265	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	338	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 266	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	339	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 267	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	340	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 268	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	341	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 269	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	342	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 270	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	343	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 271	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	344	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 272	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	345	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 273	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	346	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 274	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	347	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 275	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	348	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 276	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	349	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 277	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	350	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 278	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	351	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 279	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	352	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 280	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	353	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 281	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	354	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 282	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	355	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 283	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	356	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 284	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	357	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 285	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	358	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 286	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	359	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 287	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	360	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 288	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	361	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 289	9.6	50.5	19	14	ADU64854	Adu64854 Human MAP	362	9.4	49.5	19	14	ADY87959	Ady87959 VEGFR b1R
C 290	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	363	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 291	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	364	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 292	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	365	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 293	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	366	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 294	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	367	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 295	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	368	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 296	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	369	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 297	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	370	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 298	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	371	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 299	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	372	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 300	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	373	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 301	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	374	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 302	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	375	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 303	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	376	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 304	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	377	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 305	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	378	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 306	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	379	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 307	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	380	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 308	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	381	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 309	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	382	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a
C 310	9.4	49.5	19	3	AAAB85547	Aaab85547 Human b1a	383	9.2	48.4	19	3	AAAB85547	Aaab85547 Human b1a

384	C	9.2	48.4	19	10	ADP93477	Adf93477	Human	TER	C	457	9.2	48.4	19	14	AEC15023	Aec15023	Human	IL-
385	C	9.2	48.4	19	10	ADH16461	Adh16461	Human	BAC	C	458	9.2	48.4	19	14	AEC15246	Aec15246	Human	IL-
386	C	9.2	48.4	19	10	ADH16786	Adh16786	Human	BAC	C	459	9.2	48.4	19	14	AEC33456	Aec33456	Human	GAB
387	C	9.2	48.4	19	11	ADL69781	Adl69781	Human	GIP	C	460	9.2	48.4	19	14	AEC33792	Aec33792	Human	GAB
388	C	9.2	48.4	19	11	ADL69821	Adl69821	Human	GIP	C	461	9.2	48.4	19	14	AEC58589	Aec58589	Human	bet
389	C	9.2	48.4	19	11	ADN34742	Adn34742	BINA	uppe	C	462	9.2	48.4	19	14	AEC58264	Aec58264	Human	bet
390	C	9.2	48.4	19	11	ADN35000	Adn35000	sINA	lowe	C	463	9.2	48.4	19	14	AEC58755	Aec58755	Human	pre
391	C	9.2	48.4	19	12	ADL91661	Adl91661	Synovial		C	464	9.2	48.4	19	14	AEC58672	Aec58672	Human	pre
392	C	9.2	48.4	19	12	ADN35855	Adn35855	Human	NSC	C	465	9.2	48.4	19	14	AED36232	Aed36232	VEGF	or V
393	C	9.2	48.4	19	12	ADN75454	Adn75454	Human	CDC	C	466	9.2	48.4	19	14	AED36659	Aed36659	VEGF	or V
394	C	9.2	48.4	19	12	ADN75379	Adn75379	Human	CD4	C	467	9.2	48.4	19	14	AED56844	Aed56844	Human	ost
395	C	9.2	48.4	19	12	ADM15882	Adm15882	Murine	SA	C	468	9.2	48.4	19	14	AED56410	Aed56410	Human	ost
396	C	9.2	48.4	19	12	ADG6267	Adg6267	Anti-Opel		C	469	9.2	48.4	19	14	AED93521	Aed93521	sRNA	low
397	C	9.2	48.4	19	13	ADQ14170	Adq14170	CAPN3/DYS		C	470	9.2	48.4	19	14	AED92130	Aed92130	Target/si	
398	C	9.2	48.4	19	13	ADT04647	Adt04647	Novel	mut	C	471	9.2	48.4	19	14	AED93882	Aed93882	sRNA	low
399	C	9.2	48.4	19	13	ADT64559	Adt64559	SARS	coro	C	472	9.2	48.4	19	14	AED93876	Aed93876	sRNA	low
400	C	9.2	48.4	19	13	ADT66210	Adt66210	SARS	coro	C	473	9.2	48.4	19	14	AED91767	Aed91767	Target/si	
401	C	9.2	48.4	19	14	ADM84542	Adm84542	MAP3K9	ma	C	474	9.2	48.4	19	14	AED91771	Aed91771	Target/si	
402	C	9.2	48.4	19	14	ADV93846	Adv93846	Beta-sect		C	475	9.2	48.4	19	14	AED91772	Aed91772	Target/si	
403	C	9.2	48.4	19	14	ADV93929	Adv93929	Preseent11		C	476	9.2	48.4	19	14	AED93520	Aed93520	sRNA	low
404	C	9.2	48.4	19	14	ADV93521	Adv93521	Beta-sect		C	477	9.2	48.4	19	14	AED91769	Aed91769	Target/si	
405	C	9.2	48.4	19	14	ADV94012	Adv94012	Preseent11		C	478	9.2	48.4	19	14	AED92124	Aed92124	Target/si	
406	C	9.2	48.4	19	14	ADM78928	Adm78928	Human	ace	C	479	9.2	48.4	19	14	AED93519	Aed93519	sRNA	low
407	C	9.2	48.4	19	14	ADM79342	Adm79342	Human	ace	C	480	9.2	48.4	19	14	AED93523	Aed93523	sRNA	low
408	C	9.2	48.4	19	14	ADY02646	Ady02646	Extend	pr	C	481	9.2	48.4	19	14	AED93524	Aed93524	sRNA	low
409	C	9.2	48.4	19	14	ADY57903	Ady57903	Human	hai	C	482	9.2	48.4	19	14	AED93522	Aed93522	sRNA	low
410	C	9.2	48.4	19	14	ADY57596	Ady57596	Human	hai	C	483	9.2	48.4	19	14	AED91770	Aed91770	Target/si	
411	C	9.2	48.4	19	14	ADY50633	Ady50633	MAPK14	si	C	484	9.2	48.4	19	14	AED91768	Aed91768	Target/si	
412	C	9.2	48.4	19	14	ADY86997	Ady86997	VEGFR	sir	C	485	9.2	48.4	19	14	AEB04613	Aeb04613	Oligonuci	
413	C	9.2	48.4	19	14	ADY87424	Ady87424	VEGFR	sir	C	486	9.2	48.4	19	14	AEB54510	Aeb54510	Human	hai
414	C	9.2	48.4	19	14	ADY57931	Ady57931	Sense	sir	C	487	9.2	48.4	19	14	AEB54513	Aeb54513	Human	hai
415	C	9.2	48.4	19	14	ADY58151	Ady58151	Antisense		C	488	9.2	48.4	19	14	AEB54519	Aeb54519	Human	hai
416	C	9.2	48.4	19	14	ADZ82429	Adz82429	Method of		C	489	9.2	48.4	19	14	AEB54516	Aeb54516	Human	hai
417	C	9.2	48.4	19	14	ADZ83097	Adz83097	MPHOSPH		C	490	9.2	48.4	19	14	AEB54512	Aeb54512	Human	hai
418	C	9.2	48.4	19	14	ADZ83357	Adz83357	POLK	gene	C	491	9.2	48.4	19	14	AEB54514	Aeb54514	Human	hai
419	C	9.2	48.4	19	14	ADZ53582	Adz53582	Huntingcti		C	492	9.2	48.4	19	14	AEB54515	Aeb54515	Human	hai
420	C	9.2	48.4	19	14	ADZ53943	Adz53943	Huntingcti		C	493	9.2	48.4	19	14	AEB54521	Aeb54521	Human	hai
421	C	9.2	48.4	19	14	ADZ55334	Adz55334	Huntingcti		C	494	9.2	48.4	19	14	AEB54520	Aeb54520	Human	hai
422	C	9.2	48.4	19	14	ADZ53584	Adz53584	Huntingcti		C	495	9.2	48.4	19	14	AEB54518	Aeb54518	Human	hai
423	C	9.2	48.4	19	14	ADZ55333	Adz55333	Huntingcti		C	496	9.2	48.4	19	14	AEB54511	Aeb54511	Human	hai
424	C	9.2	48.4	19	14	ADZ53585	Adz53585	Huntingcti		C	497	9.2	48.4	19	14	AEB54517	Aeb54517	Human	hai
425	C	9.2	48.4	19	14	ADZ55336	Adz55336	Huntingcti		C	498	9.2	48.4	19	15	AEB57145	Aeb57145	Human	hai
426	C	9.2	48.4	19	14	ADZ55335	Adz55335	Huntingcti		C	499	9.2	48.4	19	15	AEB58542	Aeb58542	Human	hai
427	C	9.2	48.4	19	14	ADZ53581	Adz53581	Huntingcti		C	500	9.2	48.4	19	15	AEB57151	Aeb57151	Human	hai
428	C	9.2	48.4	19	14	ADZ55332	Adz55332	Huntingcti		C	501	9.2	48.4	19	15	AEB56789	Aeb56789	Human	hai
429	C	9.2	48.4	19	14	ADZ55337	Adz55337	Huntingcti		C	502	9.2	48.4	19	15	AEB58545	Aeb58545	Human	hai
430	C	9.2	48.4	19	14	ADZ53937	Adz53937	Huntingcti		C	503	9.2	48.4	19	15	AEB56790	Aeb56790	Human	hai
431	C	9.2	48.4	19	14	ADZ53583	Adz53583	Huntingcti		C	504	9.2	48.4	19	15	AEB56788	Aeb56788	Human	hai
432	C	9.2	48.4	19	14	ADZ55689	Adz55689	Huntingcti		C	505	9.2	48.4	19	15	AEB58897	Aeb58897	Human	hai
433	C	9.2	48.4	19	14	ADZ53580	Adz53580	Huntingcti		C	506	9.2	48.4	19	15	AEB56792	Aeb56792	Human	hai
434	C	9.2	48.4	19	14	ADZ55695	Adz55695	Huntingcti		C	507	9.2	48.4	19	15	AEB56793	Aeb56793	Human	hai
435	C	9.2	48.4	19	14	AEO5429	Aeo5429	Human	5-a	C	508	9.2	48.4	19	15	AEB58543	Aeb58543	Human	hai
436	C	9.2	48.4	19	14	AEO5566	Aeo5566	Human	5-a	C	509	9.2	48.4	19	15	AEB58544	Aeb58544	Human	hai
437	C	9.2	48.4	19	14	AEO40389	Aeo40389	Halfless		C	510	9.2	48.4	19	15	AEB58541	Aeb58541	Human	hai
438	C	9.2	48.4	19	14	AEO36396	Aeo36396	Halfless		C	511	9.2	48.4	19	15	AEB56791	Aeb56791	Human	hai
439	C	9.2	48.4	19	14	AEA98918	Aea98918	Human	Fas	C	512	9.2	48.4	19	15	AEB58540	Aeb58540	Human	hai
440	C	9.2	48.4	19	14	AEA99068	Aea99068	Human	Fas	C	513	9.2	48.4	19	15	AEB58903	Aeb58903	Human	hai
441	C	9.2	48.4	19	14	AEA11329	Aea11329	Human	ACA	C	514	9.2	48.4	19	15	AEB58297	Aeb58297	Human	rea
442	C	9.2	48.4	19	14	AEA11743	Aea11743	Human	ACA	C	515	9.2	48.4	19	15	AEB71787	Aeb71787	Human	rea
443	C	9.2	48.4	19	14	AEB05409	Aeb05409	Human	TL-	C	516	9.2	48.4	19	15	AEBF00303	Aebf00303	Human	MAP
444	C	9.2	48.4	19	14	AEB05186	Aeb05186	Human	IL-	C	517	9.2	48.4	19	15	AEB74759	Aeb74759	Human	HCV
445	C	9.2	48.4	19	14	AEB72354	Aeb72354	Human	5-a	C	518	9.2	48.4	19	15	AEBF80948	Aebf80948	Human	ANTL
446	C	9.2	48.4	19	14	AEB72491	Aeb72491	Human	5-a	C	519	9.2	48.4	19	2	AAO80817	Aao80817	ILH	gene p
447	C	9.2	48.4	19	14	AEB15734	Aeb15734	Human	tel	C	520	9.2	47.4	19	2	AAO29492	Aao29492	Hicidy1	
448	C	9.2	48.4	19	14	AEB15957	Aeb15957	Human	tel	C	521	9.2	47.4	19	2	AAO09347	Aao09347	Human	b1a
449	C	9.2	48.4	19	14	AEB25149	Aeb25149	Human	MDR	C	522	9.2	47.4	19	2	AAO208385	Aao208385	AcetA	prom
450	C	9.2	48.4	19	14	AEB24691	Aeb24691	Human	MDR	C	523	9.2	47.4	19	2	AAO201397	Aao201397	PCR	prime
451	C	9.2	48.4	19	14	AEB64194	Aeb64194	Human	IGF	C	524	9.2	47.4	19	3	AAO288621	Aao288621	Human	TRF
452	C	9.2	48.4	19	14	AEB64471	Aeb64471	Human	IGF	C	525	9.2	47.4	19	3	AAO60108	Aao60108	Primer	2
453	C	9.2	48.4	19	14	AEB54170	Aeb54170	Human	tra	C	526	9.2	47.4	19	3	AAO70741	Aao70741	PCR	prime
454	C	9.2	48.4	19	14	AEB54044	Aeb54044	Human	tra	C	527	9.2	47.4	19	3	AAO84853	Aao84853	Cyclin	F
455	C	9.2	48.4	19	14	AEB54197	Aeb54197	Human	tra	C	528	9.2	47.4	19	3	AAO85360	Aao85360	Cyclin	H
456	C	9.2	48.4	19	14	AEB54017	Aeb54017	Human	tra	C	529	9.2	47.4	19	3	AAO12248	Aao12248	Feline	hu

530	9	47.4	19	3	AAZ70070	Human	bia	C 603	9	47.4	19	12	ADN96697	Adn96697	Human	NOV
C 531	9	47.4	19	3	AAZ29625	Forward P		C 604	9	47.4	19	12	ADN96493	Adn96493	Human	NOV
C 532	9	47.4	19	4	AAH40849	SNP spec		C 605	9	47.4	19	12	ADN96430	Adn96430	Human	NOV
C 533	9	47.4	19	4	AAE26247	B. megate		C 606	9	47.4	19	12	AD044682	Ad044682	Human	oil
534	9	47.4	19	5	AAH23943	S. spiritit		C 607	9	47.4	19	12	AD018590	Ad018590	Analytica	
535	9	47.4	19	5	AAH60015	Cyclin F		C 608	9	47.4	19	12	AD018249	Ad018249	Analytica	
C 536	9	47.4	19	5	AAH60522	Cyclin H		C 609	9	47.4	19	12	AD018495	Ad018495	Analytica	
537	9	47.4	19	6	ABN88122	Caenorhab		C 610	9	47.4	19	12	AD018495	Ad018495	Analytica	
C 538	9	47.4	19	6	ABL43167	Human chr		C 611	9	47.4	19	12	AD048759	Ad048759	Human	neu
C 539	9	47.4	19	6	ABD22639	Sense PCR		C 612	9	47.4	19	12	AD062637	Ad062637	Human	neu
C 540	9	47.4	19	6	ABK82137	Novel fto		C 613	9	47.4	19	12	AD067690	Ad067690	Human	ret
C 541	9	47.4	19	8	ACC55340	Human ADA		C 614	9	47.4	19	13	ADR82672	Adr82672	Beta-acti	
C 542	9	47.4	19	8	ABT32656	Microbial		C 615	9	47.4	19	13	ADR87856	Adr87856	Human	apo
C 543	9	47.4	19	8	ABQ80061	T. marit		C 616	9	47.4	19	13	ADR77667	Adr77667	Human	apo
C 544	9	47.4	19	8	ABZ26021	PCR prime		C 617	9	47.4	19	13	ADR78517	Adr78517	Human	apo
C 545	9	47.4	19	9	ACD06573	RT-PCR pr		C 618	9	47.4	19	13	ADR79302	Adr79302	Human	apo
C 546	9	47.4	19	9	ACD06663	RT-PCR pr		C 619	9	47.4	19	13	ADR76554	Adr76554	Human	apo
C 547	9	47.4	19	9	ACD06597	RT-PCR pr		C 620	9	47.4	19	13	ADR79498	Adr79498	Human	apo
C 548	9	47.4	19	9	ACD06513	RT-PCR pr		C 621	9	47.4	19	13	ADR75899	Adr75899	Human	apo
C 549	9	47.4	19	9	ACD06534	RT-PCR pr		C 622	9	47.4	19	13	ADR81487	Adr81487	Hepatic	
C 550	9	47.4	19	9	ACD06744	RT-PCR pr		C 623	9	47.4	19	13	ADR78958	Adr78958	Human	apo
C 551	9	47.4	19	9	ACD06558	RT-PCR pr		C 624	9	47.4	19	13	ADR78062	Adr78062	Human	apo
C 552	9	47.4	19	9	ACD06801	RT-PCR pr		C 625	9	47.4	19	13	ADR78490	Adr78490	Human	apo
C 553	9	47.4	19	10	ADD00571	HCV codin		C 626	9	47.4	19	13	ADR76138	Adr76138	Human	apo
C 554	9	47.4	19	10	ADD00570	HCV codin		C 627	9	47.4	19	13	ADR76340	Adr76340	Human	apo
C 555	9	47.4	19	10	ADD00457	HCV codin		C 628	9	47.4	19	13	ADR80720	Adr80720	Human	apo
C 556	9	47.4	19	10	ADD00569	HCV codin		C 629	9	47.4	19	13	ADR75872	Adr75872	Human	apo
C 557	9	47.4	19	10	ADBE5585	Human c-f		C 630	9	47.4	19	13	ADR76115	Adr76115	SARS	coro
C 558	9	47.4	19	10	ADBE5701	Human c-f		C 631	9	47.4	19	13	ADR76464	Adr76464	SARS	coro
C 559	9	47.4	19	10	ADBE27194	Stearoyl-		C 632	9	47.4	19	13	ADR82110	Adr82110	Apoli	
C 560	9	47.4	19	10	ADBE27484	Stearoyl-		C 633	9	47.4	19	13	ADR83941	Adr83941	Apoli	
C 561	9	47.4	19	10	ADBE30433	Mitogen a		C 634	9	47.4	19	13	ADR80315	Adr80315	Apoli	
C 562	9	47.4	19	10	ADBE30224	Mitogen a		C 635	9	47.4	19	13	ADR80581	Adr80581	Apoli	
C 563	9	47.4	19	10	ADBE30405	Mitogen a		C 636	9	47.4	19	13	ADR80783	Adr80783	Apoli	
C 564	9	47.4	19	10	ADBE30196	Mitogen a		C 637	9	47.4	19	13	ADR80997	Adr80997	Apoli	
C 565	9	47.4	19	10	ADBF36673	Human VEG		C 638	9	47.4	19	13	ADR83745	Adr83745	Apoli	
C 566	9	47.4	19	10	ADBF36997	Human VEG		C 639	9	47.4	19	13	ADR85944	Adr85944	Hepatic	
C 567	9	47.4	19	10	ADBF52593	Hepatic		C 640	9	47.4	19	13	ADR82933	Adr82933	Apoli	
C 568	9	47.4	19	10	ADBF1897	Hepatic		C 641	9	47.4	19	13	ADR85163	Adr85163	Apoli	
C 569	9	47.4	19	10	ADBF2059	Hepatic		C 642	9	47.4	19	13	ADR82505	Adr82505	Apoli	
C 570	9	47.4	19	10	ADBF52597	Hepatic		C 643	9	47.4	19	13	ADR82960	Adr82960	Apoli	
C 571	9	47.4	19	10	ADBF51904	Hepatic		C 644	9	47.4	19	13	ADR80342	Adr80342	Apoli	
C 572	9	47.4	19	10	ADBF52755	Hepatic		C 645	9	47.4	19	13	ADR83401	Adr83401	Apoli	
C 573	9	47.4	19	10	ADBF52600	Hepatic		C 646	9	47.4	19	13	ADR83199	Adr83199	Apoli	
C 574	9	47.4	19	10	ADBF51901	Hepatic		C 647	9	47.4	19	13	ADR75298	Adr75298	Enterococ	
C 575	9	47.4	19	10	ADBF68298	Human ant		C 648	9	47.4	19	13	ADX16147	Adx16147	Human	DNA
576	9	47.4	19	10	ADBF68284	Human ant		C 649	9	47.4	19	13	ACL79181	ACL79181	SARS	coro
577	9	47.4	19	10	ADBF68444	Human ant		C 650	9	47.4	19	14	ADU65546	Adu65546	Human	MMP
C 578	9	47.4	19	10	ADBF68252	Human ant		C 651	9	47.4	19	14	ADU65574	Adu65574	Human	MMP
C 579	9	47.4	19	10	ADBF54402	Human GAB		C 652	9	47.4	19	14	ADU65365	Adu65365	Human	MMP
C 580	9	47.4	19	10	ADBF54546	Human GAB		C 653	9	47.4	19	14	ADU65337	Adu65337	Human	MMP
581	9	47.4	19	10	ADBF54066	Human GAB		C 654	9	47.4	19	14	ADU94227	Adu94227	Present	
C 582	9	47.4	19	10	ADBF54210	Human GAB		C 655	9	47.4	19	14	ADU94103	Adu94103	Present	
C 583	9	47.4	19	10	ADBF5176	Human ERG		C 656	9	47.4	19	14	ADU50904	Adu50904	MAPK4	si
584	9	47.4	19	10	ADBF5000	Human ERG		C 657	9	47.4	19	14	ADY81927	Ady81927	Thale-crc	
585	9	47.4	19	10	ABZ26273	Human IL4		C 658	9	47.4	19	14	ADY88250	Ady88250	VEGFR	si
C 586	9	47.4	19	10	ACG43711	PCR prime		C 659	9	47.4	19	14	ADY87926	Ady87926	VEGFR	si
C 587	9	47.4	19	10	ADU66112	Human TGF		C 660	9	47.4	19	14	ADZ01380	Adz01380	Hepatic	
588	9	47.4	19	10	ADU66300	Human TGF		C 661	9	47.4	19	14	ADZ01921	Adz01921	Hepatic	
589	9	47.4	19	11	ADL59887	Arabidops		C 662	9	47.4	19	14	ADZ02076	Adz02076	Hepatic	
590	9	47.4	19	11	ADN34250	Lower str		C 663	9	47.4	19	14	ADZ02125	Adz02125	Hepatic	
C 591	9	47.4	19	11	ADN34011	Upper str		C 664	9	47.4	19	14	ADZ02128	Adz02128	Hepatic	
C 592	9	47.4	19	11	ADN34011	Upper str		C 665	9	47.4	19	14	ADZ02131	Adz02131	Hepatic	
C 593	9	47.4	19	11	ADN34011	Upper str		C 666	9	47.4	19	14	ADZ02134	Adz02134	Hepatic	
C 594	9	47.4	19	11	ADN34011	Upper str		C 667	9	47.4	19	14	ADZ02137	Adz02137	Hepatic	
C 595	9	47.4	19	11	ADN34011	Upper str		C 668	9	47.4	19	14	ADZ02140	Adz02140	Hepatic	
C 596	9	47.4	19	11	ADN34011	Upper str		C 669	9	47.4	19	14	ADZ02143	Adz02143	Hepatic	
C 597	9	47.4	19	11	ADN34011	Upper str		C 670	9	47.4	19	14	ADZ02146	Adz02146	Hepatic	
C 598	9	47.4	19	11	ADN34011	Upper str		C 671	9	47.4	19	14	ADZ02149	Adz02149	Hepatic	
C 599	9	47.4	19	11	ADN34011	Upper str		C 672	9	47.4	19	14	ADZ02152	Adz02152	Hepatic	
C 600	9	47.4	19	11	ADN34011	Upper str		C 673	9	47.4	19	14	ADZ02155	Adz02155	Hepatic	
C 601	9	47.4	19	11	ADN34011	Upper str		C 674	9	47.4	19	14	ADZ02158	Adz02158	Hepatic	
C 602	9	47.4	19	11	ADN34011	Upper str		C 675	9	47.4	19	14	ADZ02161	Adz02161	Hepatic	

676	9	47.4	19	14	AEA09632	Aeo09632	Antisense	c 749	8.8	46.3	19	2	AAX09256	Aax09256	Human bia
c 677	9	47.4	19	14	AD254045	Ad254045	Hunt1ngt1	c 750	8.8	46.3	19	2	AAV44654	Aav44654	Primer fo
c 678	9	47.4	19	14	AD254046	Ad254046	Hunt1ngt1	c 751	8.8	46.3	19	2	AAV27773	Aav27773	Monamine
c 679	9	47.4	19	14	AD255797	Ad255797	Hunt1ngt1	c 752	8.8	46.3	19	2	AAV81899	Aav81899	Chicken t
c 680	9	47.4	19	14	AD254044	Ad254044	Hunt1ngt1	c 753	8.8	46.3	19	2	AAZ01338	Aaz01338	PCR prime
c 681	9	47.4	19	14	AD255798	Ad255798	Hunt1ngt1	c 754	8.8	46.3	19	3	AAa83550	Aa83550	cdk-we-hu
c 682	9	47.4	19	14	AD255796	Ad255796	Hunt1ngt1	c 755	8.8	46.3	19	3	AAa84005	Aa84005	Cyclin A2
c 683	9	47.4	19	14	AEA05099	Aeo05099	Human 5-a	c 756	8.8	46.3	19	3	AAa84006	Aa84006	Cyclin A2
c 684	9	47.4	19	14	AEA05222	Aeo05222	Human 5-a	c 757	8.8	46.3	19	3	AAZ73270	Aaz73270	Human bia
c 685	9	47.4	19	14	AEA9083	Aeo9083	Human 5-a	c 758	8.8	46.3	19	3	AAZ70796	Aaz70796	Human bia
c 686	9	47.4	19	14	AEA9893	Aeo9893	Human Fas	c 759	8.8	46.3	19	3	AAA75152	Aaa75152	Neocazrin
c 687	9	47.4	19	14	AEA33624	Aea33624	18S DNA r	c 760	8.8	46.3	19	3	AAF59402	Aaf59402	Human hos
c 688	9	47.4	19	14	AEb72024	Aeb72024	Human S-a	c 761	8.8	46.3	19	5	AAH59167	Aah59167	Cyclin A2
c 689	9	47.4	19	14	AEb72147	Aeb72147	Human 5-a	c 762	8.8	46.3	19	5	AAH58712	Aah58712	Cdk-we-hu
c 690	9	47.4	19	14	AEb29286	Aeb29286	Human s1r	c 763	8.8	46.3	19	5	AAH59168	Aah59168	Cyclin A2
c 691	9	47.4	19	14	AEb55101	Aeb55101	s1RNA tar	c 764	8.8	46.3	19	6	ABA95075	Aba95075	Mouse IDP
c 692	9	47.4	19	14	AEb54963	Aeb54963	s1RNA tar	c 765	8.8	46.3	19	6	ABK15585	Abk15585	Melanocor
c 693	9	47.4	19	14	AEb25898	Aeb25898	Human cyc	c 766	8.8	46.3	19	6	ABK15582	Abk15582	Melanocor
c 694	9	47.4	19	14	AEb26137	Aeb26137	Human cyc	c 767	8.8	46.3	19	6	AAJ38866	Aaj38866	Rat sense
c 695	9	47.4	19	14	AEb33459	Aeb33459	Human GAB	c 768	8.8	46.3	19	6	ABQ74945	Abq74945	Medane re
c 696	9	47.4	19	14	AEb33795	Aeb33795	Human GAB	c 769	8.8	46.3	19	6	ABH89717	Abh89717	Human ABC
c 697	9	47.4	19	14	AEb33651	Aeb33651	Human GAB	c 770	8.8	46.3	19	6	ABH89721	Abh89721	Human ABC
c 698	9	47.4	19	14	AEb33315	Aeb33315	Human GAB	c 771	8.8	46.3	19	8	ACC49453	Acc49453	Beta-acti
c 699	9	47.4	19	14	AEb58970	Aeb58970	Human pre	c 772	8.8	46.3	19	9	AB281567	Ab281567	G1a1 f1b
c 700	9	47.4	19	14	AEb58846	Aeb58846	Human pre	c 773	8.8	46.3	19	9	ACC84000	Acc84000	Beta-acti
c 701	9	47.4	19	14	AEb01394	Aeb01394	Salmonell	c 774	8.8	46.3	19	9	ADA25475	Ada25475	Human PKC
c 702	9	47.4	19	14	AEb60853	Aeb60853	Hepatit1s	c 775	8.8	46.3	19	9	ADA25350	Ada25350	Human PKC
c 703	9	47.4	19	14	AEb61546	Aeb61546	Hepatit1s	c 776	8.8	46.3	19	9	ADA27382	Ada27382	Human bet
c 704	9	47.4	19	14	AEb61704	Aeb61704	Hepatit1s	c 777	8.8	46.3	19	10	ADC46954	Adc46954	PCR prime
c 705	9	47.4	19	14	AEb61008	Aeb61008	Hepatit1s	c 778	8.8	46.3	19	10	ADC08984	Adc08984	Beta-acti
c 706	9	47.4	19	14	AEb60850	Aeb60850	Hepatit1s	c 779	8.8	46.3	19	10	ADD08997	Add08997	Human bet
c 707	9	47.4	19	14	AEb61542	Aeb61542	Hepatit1s	c 780	8.8	46.3	19	10	ADD42111	Add42111	Beta-acti
c 708	9	47.4	19	14	AEb61549	Aeb61549	Hepatit1s	c 781	8.8	46.3	19	10	ACF58143	Acf58143	Beta-acti
c 709	9	47.4	19	14	AEb60846	Aeb60846	Hepatit1s	c 782	8.8	46.3	19	10	ACF80610	Acf80610	Baculovir
c 710	9	47.4	19	14	AEb11516	Aeb11516	s1RNA use	c 783	8.8	46.3	19	10	ADE27361	Ade27361	Stearyl-1
c 711	9	47.4	19	14	AEb37485	Aeb37485	VEGF or V	c 784	8.8	46.3	19	10	ADE27071	Ade27071	Stearyl-1
c 712	9	47.4	19	14	AEb37161	Aeb37161	VEGF or V	c 785	8.8	46.3	19	10	ADE85902	Ade85902	Beta-acti
c 713	9	47.4	19	14	AEb65950	Aeb65950	Arabidops	c 786	8.8	46.3	19	10	ADE29481	Ade29481	Mitogen a
c 714	9	47.4	19	14	AEb65625	Aeb65625	Arabidops	c 787	8.8	46.3	19	10	ADE29644	Ade29644	Mitogen a
c 715	9	47.4	19	14	AEb80278	Aeb80278	Arabidops	c 788	8.8	46.3	19	10	ADD98845	Add98845	Beta-acti
c 716	9	47.4	19	14	AEb51869	Aeb51869	Human SCD	c 789	8.8	46.3	19	10	ADF35770	Adf35770	Human VEG
c 717	9	47.4	19	14	AEb52159	Aeb52159	Human SCD	c 790	8.8	46.3	19	10	ADF36197	Adf36197	Human VEG
c 718	9	47.4	19	14	AEb81157	Aeb81157	Human IRX	c 791	8.8	46.3	19	10	ADF37578	Adf37578	Human VEG
c 719	9	47.4	19	14	AEb81156	Aeb81156	Human IRX	c 792	8.8	46.3	19	10	ADF36020	Adf36020	Human VEG
c 720	9	47.4	19	14	AEb92233	Aeb92233	Target/si	c 793	8.8	46.3	19	10	ADF37331	Adf37331	Human VEG
c 721	9	47.4	19	14	AEb92232	Aeb92232	Target/si	c 794	8.8	46.3	19	10	ADF35447	Adf35447	Human VEG
c 722	9	47.4	19	14	AEb9385	Aeb9385	s1RNA low	c 795	8.8	46.3	19	10	ADF49839	Adf49839	Human BCL
c 723	9	47.4	19	14	AEb9384	Aeb9384	s1RNA low	c 796	8.8	46.3	19	10	ADF49425	Adf49425	Human BCL
c 724	9	47.4	19	14	AEb92231	Aeb92231	Target/si	c 797	8.8	46.3	19	10	ADF53752	Adf53752	Beta-acti
c 725	9	47.4	19	14	AEb93983	Aeb93983	s1RNA low	c 798	8.8	46.3	19	10	ADF75673	Adf75673	Antisense
c 726	9	47.4	19	14	AEb93429	Aeb93429	Human hai	c 799	8.8	46.3	19	10	ADF75488	Adf75488	Sense sin
c 727	9	47.4	19	14	AEb43430	Aeb43430	Human hai	c 800	8.8	46.3	19	10	ADG35350	Adg35350	HIV s1NA
c 728	9	47.4	19	15	AEb57282	Aeb57282	Human hun	c 801	8.8	46.3	19	10	ADG35353	Adg35353	HIV s1NA
c 729	9	47.4	19	15	AEb57254	Aeb57254	Human hun	c 802	8.8	46.3	19	10	ADG36068	Adg36068	HIV s1NA
c 730	9	47.4	19	15	AEb57253	Aeb57253	Human hun	c 803	8.8	46.3	19	10	ADG36071	Adg36071	HIV s1NA
c 731	9	47.4	19	15	AEb59006	Aeb59006	Human hun	c 804	8.8	46.3	19	10	ADG36088	Adg36088	HIV s1NA
c 732	9	47.4	19	15	AEb59004	Aeb59004	Human hun	c 805	8.8	46.3	19	10	ADG35320	Adg35320	HIV s1NA
c 733	9	47.4	19	15	AEb59005	Aeb59005	Human hun	c 806	8.8	46.3	19	10	ADG35330	Adg35330	HIV s1NA
c 734	9	47.4	19	15	AEb27114	Aeb27114	Arabidops	c 807	8.8	46.3	19	10	ADG35372	Adg35372	HIV s1NA
c 735	9	47.4	19	15	AEb69854	Aeb69854	Human TGF	c 808	8.8	46.3	19	10	ADG36110	Adg36110	HIV s1NA
c 736	9	47.4	19	15	AEb6982	Aeb6982	Human TGF	c 809	8.8	46.3	19	10	ADG36008	Adg36008	HIV s1NA
c 737	9	47.4	19	15	AEb08599	Aeb08599	PFTK1 s1r	c 810	8.8	46.3	19	10	ADG36059	Adg36059	HIV s1NA
c 738	9	47.4	19	15	AEb08355	Aeb08355	LOC115209	c 811	8.8	46.3	19	10	ADG35321	Adg35321	HIV s1NA
c 739	9	47.4	19	15	AEb57287	Aeb57287	Human gen	c 812	8.8	46.3	19	10	ADG35270	Adg35270	HIV s1NA
c 740	9	47.4	19	15	AEb75559	Aeb75559	Human NOG	c 813	8.8	46.3	19	10	ADG36051	Adg36051	HIV s1NA
c 741	9	47.4	19	15	AEb75785	Aeb75785	Human NOG	c 814	8.8	46.3	19	10	ADG35313	Adg35313	HIV s1NA
c 742	9	47.4	19	15	AEb73424	Aeb73424	Probe tar	c 815	8.8	46.3	19	10	ADG36058	Adg36058	HIV s1NA
c 743	9	46.3	19	15	AAO38225	Aao38225	Sequence	c 816	8.8	46.3	19	10	ADF66304	Adf66304	Beta-acti
c 744	9	46.3	19	2	AAQ39289	Aaq39289	Glucocere	c 817	8.8	46.3	19	10	ADG64623	Adg64623	Human G72
c 745	9	46.3	19	2	AAQ73605	Aaq73605	Dactylis	c 818	8.8	46.3	19	10	ADG64567	Adg64567	Human G72
c 746	9	46.3	19	2	AAQ57626	Aaq57626	PCR prime	c 819	8.8	46.3	19	11	ADL69948	Adl69948	Human GIP
c 747	9	46.3	19	2	AAI36937	Aai36937	OVCA1 gen	c 820	8.8	46.3	19	11	ADL70061	Adl70061	Human GIP
c 748	9	46.3	19	2	AAV05764	Aav05764	Chicken p	c 821	8.8	46.3	19	11	ADM77346	Adm77346	Human f1b

822	8.8	46.3	19	11	ADN34785	Adn34785 siNA Lowe	895	8.8	46.3	19	14	ADY87273	Ady87273 VEGFR siR
823	8.8	46.3	19	11	AD014826	Ad014826 Human PDG	896	8.8	46.3	19	14	ADY88584	Ady88584 VEGFR siR
824	8.8	46.3	19	11	AD015137	Ad015137 Human PDG	897	8.8	46.3	19	14	ADZ14976	Adz14976 Hydroxyme
825	8.8	46.3	19	11	ADK52852	Adk52852 siNA uppe	898	8.8	46.3	19	14	ADZ21949	Adz21949 Beta-actl
826	8.8	46.3	19	12	ADP91378	Adp91378 Primer fo	899	8.8	46.3	19	14	ADZ08451	Adz08451 Human pro
827	8.8	46.3	19	12	ADK45146	Adk45146 Human bet	900	8.8	46.3	19	14	ADZ08266	Adz08266 Human pro
828	8.8	46.3	19	12	ADH01519	Adh01519 Protein t	901	8.8	46.3	19	14	AEAO4617	AEAO4617 Human miR
829	8.8	46.3	19	12	ADH01593	Adh01593 Protein t	902	8.8	46.3	19	14	AEAO4663	AEAO4663 Human miR
830	8.8	46.3	19	12	ADH01594	Adh01594 Protein t	903	8.8	46.3	19	14	AEAO4580	AEAO4580 Human miR
831	8.8	46.3	19	12	ADP91187	Adp91187 Human bet	904	8.8	46.3	19	14	ADZ82782	Adz82782 MAPK14 ge
832	8.8	46.3	19	12	ADH51312	Adh51312 Human bet	905	8.8	46.3	19	14	ADZ82947	Adz82947 NOTCH3 ge
833	8.8	46.3	19	12	AD128749	Ad128749 Human bet	906	8.8	46.3	19	14	ADZ82705	Adz82705 Method of
834	8.8	46.3	19	12	AD128991	Ad128991 Human bet	907	8.8	46.3	19	14	AEAO5372	AEAO5372 Human 5-a
835	8.8	46.3	19	12	ADK15292	Adk15292 Human bet	908	8.8	46.3	19	14	AEAO5509	AEAO5509 Human 5-a
836	8.8	46.3	19	12	ADL27316	Adl27316 PCR prime	909	8.8	46.3	19	14	AEAO2578	AEAO2578 Cholester
837	8.8	46.3	19	12	ADL27540	Adl27540 PCR prime	910	8.8	46.3	19	14	AEAO2478	AEAO2478 Cholester
838	8.8	46.3	19	12	ADL32465	Adl32465 beta-actl	911	8.8	46.3	19	14	AEAO2127	AEAO2127 Chollnerg
839	8.8	46.3	19	12	ADL32465	Adl32465 beta-actl	912	8.8	46.3	19	14	AEAO2226	AEAO2226 Chollnerg
840	8.8	46.3	19	12	ADM94197	Adm94197 Trichoder	913	8.8	46.3	19	14	AEAO3169	AEAO3169 Hair1e88
841	8.8	46.3	19	12	ADM95240	Adm95240 DSP13.2 a	914	8.8	46.3	19	14	AEAO3476	AEAO3476 Hair1e88
842	8.8	46.3	19	12	ADN75241	Adn75241 DSP13.2 a	915	8.8	46.3	19	14	AEAO9293	AEAO9293 Human Fas
843	8.8	46.3	19	12	ADN05806	Adn05806 Beta-actl	916	8.8	46.3	19	14	AEAO9397	AEAO9397 Human Fas
844	8.8	46.3	19	12	ADN98075	Adn98075 Human bet	917	8.8	46.3	19	14	AEAA4569	AEAA4569 Human TRP
845	8.8	46.3	19	12	AD016066	Ad016066 4 syntheis	918	8.8	46.3	19	14	AEAA34645	AEAA34645 Human TRP
846	8.8	46.3	19	12	AD022062	Ad022062 Beta-actl	919	8.8	46.3	19	14	AEAA30961	AEAA30961 Human bet
847	8.8	46.3	19	12	ADQ37946	Adq37946 RNA Inter	920	8.8	46.3	19	14	AEAA11772	AEAA11772 Human ACA
848	8.8	46.3	19	12	AD085736	Ad085736 Human bet	921	8.8	46.3	19	14	AEAA11358	AEAA11358 Human ACA
849	8.8	46.3	19	12	ADQ061355	Adq061355 Anti-CD7	922	8.8	46.3	19	14	AEBO6565	AEBO6565 Human con
850	8.8	46.3	19	12	ADQ60821	Adq60821 Anti-INSR	923	8.8	46.3	19	14	AEBO6393	AEBO6393 Human con
851	8.8	46.3	19	12	ADQ62246	Adq62246 Anti-PLCG	924	8.8	46.3	19	14	AEBI17752	AEBI17752 G72 siRNA
852	8.8	46.3	19	12	ADQ61190	Adq61190 Anti-PEC	925	8.8	46.3	19	14	AEBI17696	AEBI17696 G72 siRNA
853	8.8	46.3	19	13	ADRA4800	Adra4800 Human hC4	926	8.8	46.3	19	14	AEBO3972	AEBO3972 Human ref
854	8.8	46.3	19	13	ADRA4802	Adra4802 Human hC4	927	8.8	46.3	19	14	AEBO72297	AEBO72297 Human 5-a
855	8.8	46.3	19	13	ADRA7497	Adra7497 Human bet	928	8.8	46.3	19	14	AEBA29234	AEBA29234 Human siR
856	8.8	46.3	19	13	ADRA3775	Adra3775 MLL seprct	929	8.8	46.3	19	14	AEBA70744	AEBA70744 Beta-actl
857	8.8	46.3	19	13	ADR76668	Adr76668 Human apo	930	8.8	46.3	19	14	AEBC90787	AEBC90787 STAT-3 si
858	8.8	46.3	19	13	ADR79612	Adr79612 Human apo	931	8.8	46.3	19	14	AEBC90724	AEBC90724 STAT-3 si
859	8.8	46.3	19	13	ADT63932	Adt63932 SARS coro	932	8.8	46.3	19	14	AEBA24676	AEBA24676 Human MDR
860	8.8	46.3	19	13	ADT64837	Adt64837 SARS coro	933	8.8	46.3	19	14	AEBS4915	AEBS4915 siRNA tar
861	8.8	46.3	19	13	ADT65583	Adt65583 SARS coro	934	8.8	46.3	19	14	AEBA42816	AEBA42816 Sna1l tra
862	8.8	46.3	19	13	ADT63186	Adt63186 SARS coro	935	8.8	46.3	19	14	AEBS0787	AEBS0787 Human ADA
863	8.8	46.3	19	13	ADT63170	Adt63170 SARS coro	936	8.8	46.3	19	14	AEBS0983	AEBS0983 Human ADA
864	8.8	46.3	19	13	ADT64900	Adt64900 SARS coro	937	8.8	46.3	19	14	AEBA6336	AEBA6336 Human bet
865	8.8	46.3	19	13	ADT63225	Adt63225 SARS coro	938	8.8	46.3	19	14	AEBA71654	AEBA71654 Human PKC
866	8.8	46.3	19	13	ADT64886	Adt64886 SARS coro	939	8.8	46.3	19	14	AEBA71779	AEBA71779 Human PKC
867	8.8	46.3	19	13	ADT65588	Adt65588 SARS coro	940	8.8	46.3	19	14	AEBC90510	AEBC90510 STAT-3 si
868	8.8	46.3	19	13	ADT63937	Adt63937 SARS coro	941	8.8	46.3	19	14	AEBC90787	AEBC90787 STAT-3 si
869	8.8	46.3	19	13	ADT64821	Adt64821 SARS coro	942	8.8	46.3	19	14	AEBC90724	AEBC90724 STAT-3 si
870	8.8	46.3	19	13	ADT63249	Adt63249 SARS coro	943	8.8	46.3	19	14	AEBC90446	AEBC90446 STAT-3 si
871	8.8	46.3	19	13	ADT81111	Adt81111 Apolipoptr	944	8.8	46.3	19	14	AEBC90696	AEBC90696 STAT-3 si
872	8.8	46.3	19	13	ADT84055	Adt84055 Apolipoptr	945	8.8	46.3	19	14	AEBC90418	AEBC90418 STAT-3 si
873	8.8	46.3	19	14	ADU64785	Adu64785 Human MAP	946	8.8	46.3	19	14	AEBC90418	AEBC90418 siRNA tar
874	8.8	46.3	19	14	ADU65853	Adu65853 Human MAP	947	8.8	46.3	19	14	AEBC6935	AEBC6935 VEGF or V
875	8.8	46.3	19	14	ADU66034	Adu66034 Human MAP	948	8.8	46.3	19	14	AEBC6258	AEBC6258 VEGF or V
876	8.8	46.3	19	14	ADU64622	Adu64622 Human MAP	949	8.8	46.3	19	14	AEBC6685	AEBC6685 VEGF or V
877	8.8	46.3	19	14	ADU85616	Adu85616 MAP3K9 ma	950	8.8	46.3	19	14	AEBC7819	AEBC7819 VEGF or V
878	8.8	46.3	19	14	ADW27813	Adw27813 Chollnerg	951	8.8	46.3	19	14	AEBC8066	AEBC8066 VEGF or V
879	8.8	46.3	19	14	ADW27714	Adw27714 Chollnerg	952	8.8	46.3	19	14	AEBC8066	AEBC8066 VEGF or V
880	8.8	46.3	19	14	ADW79371	Adw79371 Human ace	953	8.8	46.3	19	14	AEBC6508	AEBC6508 VEGF or V
881	8.8	46.3	19	14	ADW78957	Adw78957 Human ace	954	8.8	46.3	19	14	AEBC4056	AEBC4056 VEGF or V
882	8.8	46.3	19	14	ADY02581	Ady02581 Extend pr	955	8.8	46.3	19	14	AEBC76469	AEBC76469 Rat PNP65
883	8.8	46.3	19	14	ADY03112	Ady03112 Extend pr	956	8.8	46.3	19	14	AEBC76468	AEBC76468 Rat PNP65
884	8.8	46.3	19	14	ADX86554	Adx86554 XIAP tarq	957	8.8	46.3	19	14	AEBC76567	AEBC76567 Human ga1
885	8.8	46.3	19	14	ADX86661	Adx86661 XIAP tarq	958	8.8	46.3	19	14	AEBC17466	AEBC17466 Human ga1
886	8.8	46.3	19	14	ADX86194	Adx86194 XIAP tarq	959	8.8	46.3	19	14	AEBC52036	AEBC52036 Human SCD
887	8.8	46.3	19	14	ADX87021	Adx87021 XIAP tarq	960	8.8	46.3	19	14	AEBC18111	AEBC18111 Human bet
888	8.8	46.3	19	14	ADY57683	Ady57683 Human hai	961	8.8	46.3	19	14	AEBS3622	AEBS3622 Human hai
889	8.8	46.3	19	14	ADY57376	Ady57376 Human hai	962	8.8	46.3	19	14	AEBS3622	AEBS3622 Human hai
890	8.8	46.3	19	14	ADY50909	Ady50909 MAPK14 si	963	8.8	46.3	19	14	AEBA43131	AEBA43131 Human hai
891	8.8	46.3	19	14	ADY87023	Ady87023 VEGFR siR	964	8.8	46.3	19	14	AEBA43135	AEBA43135 Human hai
892	8.8	46.3	19	14	ADY87450	Ady87450 VEGFR siR	965	8.8	46.3	19	14	AEBA46726	AEBA46726 Human hai
893	8.8	46.3	19	14	ADY87700	Ady87700 VEGFR siR	966	8.8	46.3	19	14	AEBA43145	AEBA43145 Human hai
894	8.8	46.3	19	14	ADY88831	Ady88831 VEGFR siR	967	8.8	46.3	19	14	AEBA43132	AEBA43132 Human hai

968	8.8	46.3	19	14	AEE43133	Aee43133 Human hai
C 969	8.8	46.3	19	14	AEE43142	Aee43142 Human hai
C 970	8.8	46.3	19	14	AEE46725	Aee46725 Human hai
C 971	8.8	46.3	19	14	AEE43138	Aee43138 Human hai
C 972	8.8	46.3	19	14	AEE46707	Aee46707 Human hai
C 973	8.8	46.3	19	14	AEE46708	Aee46708 Human hai
C 974	8.8	46.3	19	14	AEE53638	Aee53638 Human hai
C 975	8.8	46.3	19	14	AEE53639	Aee53639 Human hai
C 976	8.8	46.3	19	14	AEE43140	Aee43140 Human hai
C 977	8.8	46.3	19	14	AEE43144	Aee43144 Human hai
C 978	8.8	46.3	19	14	AEE53623	Aee53623 Human hai
C 979	8.8	46.3	19	14	AEE43137	Aee43137 Human hai
C 980	8.8	46.3	19	14	AEE43139	Aee43139 Human hai
C 981	8.8	46.3	19	14	AEE43141	Aee43141 Human hai
C 982	8.8	46.3	19	14	AEE43136	Aee43136 Human hai
C 983	8.8	46.3	19	14	AEE43143	Aee43143 Human hai
C 984	8.8	46.3	19	14	AEE43146	Aee43146 Human hai
C 985	8.8	46.3	19	15	AEE61132	Aee61132 Human C-J
C 986	8.8	46.3	19	15	AEE700383	Aee700383 Human MAP
C 987	8.8	46.3	19	15	AEE14461	Aee14461 Human cho
C 988	8.8	46.3	19	15	AEE37645	Aee37645 Human PTP
C 989	8.8	46.3	19	15	AEE37460	Aee37460 Human PTP
C 990	8.8	46.3	19	15	AEE58501	Aee58501 Human bet
C 991	8.8	46.3	19	15	AEE67482	Aee67482 Human PTP
C 992	8.8	46.3	19	15	AEE66884	Aee66884 Human PTP
C 993	8.8	46.3	19	15	AEE80060	Aee80060 Human bet
C 994	8.6	45.3	19	2	AAQ77689	AAQ77689 MTG8-2 pr
C 995	8.6	45.3	19	2	AAQ75022	AAQ75022 PCR prime
C 996	8.6	45.3	19	2	AAQ88258	AAQ88258 Neisseria
C 997	8.6	45.3	19	2	AAQ81240	AAQ81240 Ribozyme
C 998	8.6	45.3	19	2	AAT08591	Aat08591 K-ras pro
C 999	8.6	45.3	19	2	AAT45034	Aat45034 Carboxype
1000	8.6	45.3	19	2	AAV59355	AAV59355 Human MDR

ALIGNMENTS

RESULT 1	
ID	ABK93682
AC	ABK93682 standard; DNA; 19 BP.
XX	ABK93682;
DT	26-AUG-2002 (first entry)
DE	Human inhibitor of apoptosis, XIAP, antisense oligonucleotide #29.
XX	
KW	Human; ss; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW	cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW	pancreatic cancer; embryonic development; viral pathogenesis;
KW	autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW	lupus erythematosus; herpes virus infection; pox virus infection;
KW	adenovirus infection; proliferative disease.
XX	
OS	Homo sapiens.
XX	
PN	WO200226968-A2.
XX	
PD	04-APR-2002.
XX	
PF	27-SEP-2001; 2001WO-CA001379.
XX	
PR	28-SEP-2000; 2000US-00672717.
XX	
PA	(UYOT-) UNTV OTTAMA.
XX	(AEGE-) AEGERA THERAPEUTICS INC.
XX	
PI	Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX	
DR	WPI; 2002-479562/51.
XX	
PT	Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing

PT	apoptosis in a cell, for treating cancer and other proliferative
PT	diseases.
XX	
PS	Claim 8; Page 33; 135pp; English.
XX	
CC	The invention relates to an inhibitor of apoptosis (IAP) antisense
CC	nucleic acid (I) that inhibits IAP biological activity, regardless of
CC	length of the antisense nucleic acid, the IAP proteins may be mouse or
CC	human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC	composition comprising a mammalian IAP antisense molecule and a method of
CC	enhancing apoptosis in a cell, comprising administering a negative
CC	regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC	antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC	mammal diagnosed with a proliferative disease. The method is useful for
CC	treating a patient diagnosed with a proliferative disease like cancer.
CC	The IAP antisense molecule is useful to treat, ameliorate, improve,
CC	sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC	adenocarcinoma, lymphoma, pancreatic cancer.) and also in diseases or
CC	conditions where apoptosis is involved or implicated (e.g. embryonic
CC	development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC	diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC	virus, pox virus and adenovirus). The present sequence is an IAP
CC	antisense molecule of the invention
XX	
SQ	Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 19; DB 6; Length 19;
Best Local Similarity	100.0%; Pred. No. 5.7;
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGACGGTATCTCTTCAC 19
Db 1 CGACGGTATCTCTTCAC 19

RESULT 2	
ID	AEA10008
AC	AEA10008 standard; DNA; 19 BP.
XX	AEA10008;
DT	14-JUL-2005 (first entry)
DE	Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 29.
XX	
KW	Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO2005042030-A1.
XX	
PD	12-MAY-2005.
XX	
PF	29-OCT-2004; 2004WO-CA001900.
XX	
PR	30-OCT-2003; 2003US-0516263P.
XX	
PA	(AEGE-) AEGERA THERAPEUTICS INC.
XX	
PI	Lacasse E, Mcmanus D, Durkin JP;
XX	
DR	WPI; 2005-366517/37.
XX	
PT	Treating proliferative disease such as hepatoma, bile duct carcinoma,
PT	choilocarcinoma, seminoma and embryonal carcinoma comprises administering
PT	antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
PT	agent.
XX	
PS	Claim 6; SEQ ID NO 29; 285pp; English.
XX	
CC	The invention relates to a method of treating a patient having a
CC	proliferative disease, comprising administering to the patient, an

CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
CC chemotherapeutic agent, in amounts that together are sufficient to treat
CC the patient. The method is useful for treating a patient having a
CC proliferative disease. The proliferative disease is cancer. A composition
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
CC human cancer cell in vivo or ex vivo, which involves contacting the cell
CC with the composition. The present sequence represents an antisense
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
CC sequence represents either T or U. There are multiple versions of this
CC shown in the main body of the specification.

XX SQ Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 19; DB 14; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 5.7;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAGGATATCTCCTTCAC 19
Db 1 CGCAGGATATCTCCTTCAC 19

RESULT 3
AEA10086
ID AEA10086 standard; DNA; 19 BP.
XX
AC AEA10086;
XX
DT 14-JUL-2005 (first entry)
XX
DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 107.
XX
KM Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..3
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER = 2'-O-methyl X RNA"
FT modified_base 17..19
FT /tag= b
FT /mod_base= OTHER
FT /note= "OTHER = 2'-O-methyl X RNA"
XX
PN WO2005042030-A1.
XX
PD 12-MAY-2005.
XX
PF 29-OCT-2004; 2004WO-CA001900.
XX
PR 30-OCT-2003; 2003US-0516263P.
XX
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Lacasase E, Mcmanus D, Durkin JP;
XX
DR WPI; 2005-366517/37.
XX
PT Treating proliferative disease such as hepatoma, bile duct carcinoma,
PT chorioepithelioma, seminoma and embryonal carcinoma comprising administering
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
PT agent.
XX
PS Example 1; SEQ ID NO 107; 285bp; English.
XX
XX The invention relates to a method of treating a patient having a
XX proliferative disease, comprising administering to the patient, a
XX antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a

CC chemotherapeutic agent, in amounts that together are sufficient to treat
CC the patient. The method is useful for treating a patient having a
CC proliferative disease. The proliferative disease is cancer. A composition
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
CC human cancer cell in vivo or ex vivo, which involves contacting the cell
CC with the composition. The present sequence represents an antisense
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
CC sequence represents either T or U. There are multiple versions of this
CC shown in the main body of the specification.

XX SQ Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 19; DB 14; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 5.7;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAGGATATCTCCTTCAC 19
Db 1 CGCAGGATATCTCCTTCAC 19

RESULT 4
ADX86146/c
ID ADX86146 standard; RNA; 19 BP.
XX
AC ADX86146;
XX
DT 05-MAY-2005 (first entry)
XX
DE XIAP targeting siRNA SEQ ID NO 17.
XX
KM dg; primer; short interfering RNA; siRNA;
KM X-linked inhibitor of apoptosis protein; XIAP; RNA interference; RNAi;
KM cytostatic; cancer; gene silencing.
XX
OS Synthetic.
XX
PN WO2005014811-A2.
XX
PD 17-FEB-2005.
XX
PF 06-AUG-2004; 2004WO-US025589.
XX
PR 08-AUG-2003; 2003US-0493561P.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswigen J, Chowrira BW;
XX
DR WPI; 2005-163247/17.
XX
PT New chemically synthesized double stranded short interfering nucleic acid
PT that directs cleavage of an X-linked inhibitor of apoptosis protein
PT (XIAP) RNA via RNA interference, useful in preparing a composition for
PT treating cancer.
XX
PS Claim 33; SEQ ID NO 17, 202pp; English.
XX
XX This invention describes novel chemically synthesized double stranded
XX short interfering nucleic acid (siRNA) molecules which direct cleavage of
XX a X-linked inhibitor of apoptosis protein (XIAP) RNA via RNA interference
XX (RNAi), where each strand of the siRNA molecule is about 18-23

OS	Homo sapiens.
XX	
XX	
XX	Key
XX	Location/Qualifiers
XX	1. 19
XX	misc_feature
XX	/*tag= a
XX	/note= "N = T or U where each nucleobase may be part of a
XX	ribonucleotide, deoxyribonucleotide, or nucleotide
XX	analogue"
XX	
XX	
XX	WO2003080638-A2.
XX	
XX	02-OCT-2003.
XX	
XX	27-MAR-2003; 2003WO-IB001670.
XX	
XX	27-MAR-2002; 2002US-0367853P.
XX	
XX	(ABGE-) ABGERRA THERAPEUTICS INC.
XX	
XX	Lacasease E, Mcmanus D, Durkin JP;
XX	WPI, 2003-779241/73.
XX	
XX	New nucleobase oligomers that inhibit expression of inhibitor of
XX	apoptosis gene, useful for treating cancer and other lymphoproliferative
XX	disorders by inducing apoptosis.
XX	
XX	Claim 54; SEQ ID NO 29; 259pp; English.
XX	
XX	The present invention describes a substantially pure nucleobase oligomer
XX	(I) of up to 30 nucleobases in length or comprising eleven DNA residues
XX	flanked on each side by four 2'-O-methyl RNA residues that inhibits the
XX	expression of an inhibitor-of apoptosis (IAP) in the cell. Also
XX	described: (1) a pharmaceutical composition (II) comprising (I) and a
XX	carrier; (2) a catalytic RNA molecule (III) capable of cleaving XIAP,
XX	HiAP1, or HiAP2 mRNA; (3) an expression vector (IV) comprising a nucleic
XX	acid encoding one or more (III) positioned for expression in a mammalian
XX	cell; (4) a double-stranded RNA molecule (IV) consisting of 21-29
XX	nucleobases, comprising at least eight consecutive nucleobases
XX	corresponding to a sequence comprising 19 nucleotides, as given in
XX	specification; (5) a double-stranded hairpin RNA molecule (V) consisting
XX	of 50-70 nucleobases, comprising a first domain of 21-29 nucleobases that
XX	comprise at least eight consecutive nucleobases corresponding to a
XX	sequence fully defined in the specification, comprising, e.g. 19
XX	nucleotides, and a second domain complementary to the first domain, and a
XX	loop domain situated between the first and the second domains such that
XX	the first domain and the second domain are capable of duplexing to form
XX	the double-stranded hairpin RNA molecule; and (6) an expression vector
XX	(VI) comprising a nucleic acid molecule encoding the double stranded RNA
XX	molecule positioned for expression in a mammalian cell. (I) has
XX	cytosstatic activity, and can be used in antisense therapy. (I) is
XX	useful for enhancing the apoptosis of a cell in an animal, preferably human
XX	where (I) inhibits the expression of an IAP in the cell. (I) is also
XX	useful for treating an animal having a cancer or lymphoproliferative
XX	disorder. The cancer includes acute leukemia, acute lymphocytic
XX	leukemia, acute myelocytic leukemia, acute myeloblastic leukemia,
XX	acute promyelocytic leukemia, acute myelomonocytic leukemia, acute
XX	monocytic leukemia, acute erythroleukemia, chronic leukemia, chronic
XX	myelocytic leukemia, myelodysplastic syndrome, chronic lymphocytic
XX	leukemia, polycythemia vera, lymphoma, Hodgkin's disease, Waldenstrom's
XX	macroglobulinemia, breast cancer, basal cell carcinoma, lung carcinoma,
XX	melanoma and retinoblastoma. The present sequence is used in the
XX	exemplification of the present invention.
XX	
XX	Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;
XX	
XX	Query Match 73.7%; Score 14; DB 10; Length 19;
XX	Best Local Similarity 73.7%; Pred. No. 2.4e+03;
XX	Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0
XX	
XX	1 CGCAGCGTATCTCTTTCAC 19
XX	
XX	1 CGCAGCGNANCCNNAC 19
XX	

CC	XX	DE	Human antisense IAP nucleobase oligomer SEQ ID NO:107.
CC	XX	KW	nucleobase oligomer; inhibitor-of apoptosis inhibitor; IAP inhibitor;
CC	XX	KW	cytostatic; antisense therapy; apoptosis enhancer; cancer;
CC	XX	KW	lymphoproliferative disorder; leukaemia; myelodysplastic syndrome;
CC	XX	KW	polycythaemia vera; lymphoma; Hodgkin's disease; basal cell carcinoma;
CC	XX	KW	Waldenstrom's macroglobulinemia; breast cancer; lung carcinoma;
CC	XX	KW	lung carcinoma; melanoma; retinoblastoma; human; ss.
CC	XX	OS	Synthetic.
CC	XX	OS	Homo sapiens.
CC	XX	PH	Key
CC	XX	PH	misc_feature
CC	XX	FT	Location/Qualifiers
CC	XX	FT	1..19
CC	XX	FT	/*reg= a
CC	XX	FT	/note= "N = T or U where each nucleobase may be part of a
CC	XX	FT	ribonucleotide, deoxyribonucleotide, or nucleotide
CC	XX	FT	analogue"
CC	XX	PX	WO2003080638-A2.
CC	XX	PD	02-OCT-2003.
CC	XX	PD	27-MAR-2003; 2003WO-IB001670.
CC	XX	PF	27-MAR-2002; 2002US-0367853P.
CC	XX	PR	(ABGE-) ABGERRA THERAPEUTICS INC.
CC	XX	PA	Lacasse E, Momannus D, Durkin JP;
CC	XX	PI	WPI, 2003-779241/73.
CC	XX	DR	New nucleobase oligomers that inhibit expression of inhibitor of
CC	XX	PT	apoptosis gene, useful for treating cancer and other Lymphoproliferative
CC	XX	PT	disorders by inducing apoptosis.
CC	XX	PS	Claim 54; SEQ ID NO 107; 25pp; English.
CC	XX	CC	The present invention describes a substantially pure nucleobase oligomer
CC	XX	CC	(I) of up to 30 nucleobases in length or comprising eleven DNA residues
CC	XX	CC	flanked on each side by four 2'-O-methyl RNA residues that inhibits the
CC	XX	CC	expression of an inhibitor of apoptosis (IAP) in the cell. Also
CC	XX	CC	described: (1) a pharmaceutical composition (II) comprising (I) and a
CC	XX	CC	carrier; (2) a catalytic RNA molecule (III) capable of cleaving XIAP,
CC	XX	CC	HMAP1, or HMAP2 mRNA; (3) an expression vector (IV) comprising a nucleic
CC	XX	CC	acid encoding one or more (III) positioned for expression in a mammalian
CC	XX	CC	cell; (4) a double-stranded RNA molecule (V) consisting of 21-29
CC	XX	CC	nucleobases, comprising at least eight consecutive nucleobases
CC	XX	CC	corresponding to a sequence comprising 19 nucleotides, as given in
CC	XX	CC	specification; (5) a double-stranded hairpin RNA molecule (V) consisting
CC	XX	CC	of 50-70 nucleobases, comprising a first domain of 21-29 nucleobases that
CC	XX	CC	comprise at least eight consecutive nucleobases corresponding to a
CC	XX	CC	sequence fully defined in the specification, comprising, e.g. 19
CC	XX	CC	nucleotides, and a second domain complementary to the first domain, and a
CC	XX	CC	loop domain situated between the first and the second domains such that
CC	XX	CC	the first domain and the second domain are capable of duplexing to form
CC	XX	CC	the double-stranded hairpin RNA molecule; and (6) an expression vector
CC	XX	CC	(VI) comprising a nucleic acid molecule encoding the double stranded RNA
CC	XX	CC	molecule positioned for expression in a mammalian cell. (I) has
CC	XX	CC	cytotoxic activity, and can be used in antisense therapy. (I) is useful
CC	XX	CC	for enhancing the apoptosis of a cell in an animal, preferably human
CC	XX	CC	where (I) inhibits the expression of an IAP in the cell. (I) is also

CC useful for treating an animal having a cancer or lymphoproliferative
 CC disorder. The cancer includes acute leukaemia, acute lymphocytic
 CC leukemia, acute myelocytic leukemia, acute myeloblastic leukemia,
 CC acute promyelocytic leukemia, acute myelomonocytic leukemia, acute
 CC monocytic leukemia, acute erythroleukemia, chronic leukemia, chronic
 CC myelocytic leukemia, myelodysplastic syndrome, chronic lymphocytic
 CC leukemia, polycythemia vera, lymphoma, Hodgkin's disease, Waldenstrom's
 CC macroglobulinemia, breast cancer, basal cell carcinoma, lung carcinoma,
 CC melanoma and retinoblastoma. The present sequence is used in the
 CC exemplification of the present invention.

XX Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;

XX Query Match 73.7%; Score 14; DB 10; Length 19;

XX Best Local Similarity 73.7%; Pred. No. 2.4e+03; Mismatches 0; Gaps 0;

XX Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTCAC 19
 |||||
 DB 1 CGCAGCGANANCNCCAC 19

RESULT 8
 ID AEA10122 standard; DNA; 19 BP.

XX AEA10122;

XX 14-JUL-2005 (first entry)

XX Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 143.

XX Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..4

FT /tag= a

FT /mod_base= OTHER

FT /note= "OTHER = 2'-O-methyl X RNA"

FT modified_base 16..19

FT /tag= b

FT /mod_base= OTHER

FT /note= "OTHER = 2'-O-methyl X RNA"

XX WO2005042030-A1.

XX 12-MAY-2005.

XX 29-OCT-2004; 2004WO-CA001900.

XX 30-OCT-2003; 2003US-0516263P.

XX (AEGE-) AEGERA THERAPEUTICS INC.

XX Lacasease E, Mcmannus D, Durkin JP;

XX WPI; 2005-366517/37.

XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
 PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering
 PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
 PT agent.

XX Claim 6; SEQ ID NO 143; 285pp; English.

XX The invention relates to a method of treating a patient having a
 CC proliferative disease, comprising administering to the patient, an
 CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
 CC chemotherapeutic agent, in amounts that together are sufficient to treat
 CC the patient. The method is useful for treating a patient having a

CC proliferative disease. The proliferative disease is cancer. A composition
 CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
 CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
 CC human cancer cell in vivo or ex vivo, which involves contacting the cell
 CC with the composition. The present sequence represents an antisense
 CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
 CC sequence represents either T or U. There are multiple versions of this
 CC sequence in the patent, the present sequence represents the sequence
 CC shown in the main body of the specification.

XX Sequence 19 BP; 4 A; 6 C; 3 G; 4 T; 2 U; 0 Other;

XX Query Match 73.7%; Score 14; DB 14; Length 19;

XX Best Local Similarity 92.9%; Pred. No. 2.4e+03; Mismatches 0; Gaps 0;

QY 6 GGTATCTCTCTTCAC 19
 |||||
 DB 1 GGATCTCTCTTCAC 14

RESULT 9
 ID AEA10076 standard; DNA; 19 BP.

XX AEA10076;

XX 14-JUL-2005 (first entry)

XX Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 97.

XX Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..2

FT /tag= a

FT /mod_base= OTHER

FT /note= "OTHER = 2'-O-methyl X RNA"

FT modified_base 18..19

FT /tag= b

FT /mod_base= OTHER

FT /note= "OTHER = 2'-O-methyl X RNA"

XX WO2005042030-A1.

XX 12-MAY-2005.

XX 29-OCT-2004; 2004WO-CA001900.

XX 30-OCT-2003; 2003US-0516263P.

XX (AEGE-) AEGERA THERAPEUTICS INC.

XX Lacasease E, Mcmannus D, Durkin JP;

XX WPI; 2005-366517/37.

XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
 PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering
 PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
 PT agent.

XX Claim 6; SEQ ID NO 97; 285pp; English.

XX The invention relates to a method of treating a patient having a
 CC proliferative disease, comprising administering to the patient, an
 CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
 CC chemotherapeutic agent, in amounts that together are sufficient to treat
 CC the patient. The method is useful for treating a patient having a
 CC proliferative disease. The proliferative disease is cancer. A composition

CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
CC human cancer cell in vivo or ex vivo, which involves contracting the cell
CC with the composition. The present sequence represents an antisense
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
CC sequence represents either T or U. There are multiple versions of this
CC sequence in the patent, the present sequence represents the sequence
CC shown in the main body of the specification.
XX
SQ Sequence 19 BP; 4 A; 6 C; 3 G; 5 T; 1 U; 0 Other;
XX
Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 GGATCTCTCTTAC 19
1 GGATCTCTCTTAC 14
XX
RESULT 10
ID AEA10108 standard; DNA; 19 BP.
XX
AC AEA10108;
XX
DT 14-JUL-2005 (first entry)
XX
DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 129.
XX
KW Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
XX
OS Homo sapiens.
XX
SN Synthetic.
XX
PN WO2005042030-A1.
XX
PD 12-MAY-2005.
XX
PF 29-OCT-2004; 2004WO-CA001900.
XX
PR 30-OCT-2003; 2003US-0516263P.
XX
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Lacasease E, Mcmanus D, Durkin JP;
XX
PI Lacasease E, Mcmanus D, Durkin JP;
XX
DR WPI; 2005-366517/37.
XX
PT Treating proliferative disease such as hepatoma, bile duct carcinoma,
PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
PT agent.
XX
PS Example 1; SEQ ID NO 129; 285bp; English.
XX
CC The invention relates to a method of treating a patient having a
CC proliferative disease, comprising administering to the patient, an
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
CC chemotherapeutic agent, in amounts that together are sufficient to treat
CC the patient. The method is useful for treating a patient having a
CC proliferative disease. The proliferative disease is cancer. A composition
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
CC human cancer cell in vivo or ex vivo, which involves contracting the cell
CC with the composition. The present sequence represents an antisense
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
CC sequence represents either T or U. There are multiple versions of this
CC sequence in the patent, the present sequence represents the sequence
CC shown in the main body of the specification.
XX
SQ Sequence 19 BP; 4 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 GGATCTCTCTTAC 19
1 GGATCTCTCTTAC 14
XX
Db 1 GGATCTCTCTTAC 14
XX
RESULT 11
ID AEA09518 standard; DNA; 19 BP.
XX
AC AEA09518;
XX
DT 14-JUL-2005 (first entry)
XX
DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 29.
XX
KW Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
XX
OS Homo sapiens.
XX
SN Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..19
FT /*tag= a
FT /note= "The residues represented by N are either T or U"
XX
PN WO2005042030-A1.
XX
PD 12-MAY-2005.
XX
PF 29-OCT-2004; 2004WO-CA001900.
XX
PR 30-OCT-2003; 2003US-0516263P.
XX
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Lacasease E, Mcmanus D, Durkin JP;
XX
PI Lacasease E, Mcmanus D, Durkin JP;
XX
DR WPI; 2005-366517/37.
XX
PT Treating proliferative disease such as hepatoma, bile duct carcinoma,
PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
PT agent.
XX
PS Claim 6; SEQ ID NO 29; 285bp; English.
XX
CC The invention relates to a method of treating a patient having a
CC proliferative disease, comprising administering to the patient, an
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
CC chemotherapeutic agent, in amounts that together are sufficient to treat
CC the patient. The method is useful for treating a patient having a
CC proliferative disease. The proliferative disease is cancer. A composition
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
CC human cancer cell in vivo or ex vivo, which involves contracting the cell
CC with the composition. The present sequence represents an antisense
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
CC sequence represents either T or U. There are multiple versions of this
CC sequence in the patent, the present sequence represents the sequence
CC shown in the main body of the specification.
XX
SQ Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;
XX
Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 1 CGCAGGATCTCTCTTAC 19
1 CGCAGGATCTCTCTTAC 19

DB 1 CGCAGCGNANCCNNCAC 19

RESULT 12
AEA10267
ID AEA10267 standard; DNA; 19 BP.
XX
XX AEA10267;
AC
XX
DT 14-JUL-2005 (first entry)
XX
XX Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 289.
DE
XX Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
KM
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO2005042030-A1.
PN
XX 12-MAY-2005.
PD
XX 29-OCT-2004; 2004WO-CA001900.
PF
XX 30-OCT-2003; 2003US-0516263P.
PR
XX (AEGE-) AEGERA THERAPEUTICS INC.
PA
XX Lacase E, Mcmanus D, Durkin JP;
PI
XX WPI; 2005-366517/37.
DR
XX
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
PT agent.
XX
XX Claim 6; SEQ ID NO 289; 285pp; English.
PS
XX
XX The invention relates to a method of treating a patient having a
CC proliferative disease, comprising administering to the patient, an
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
CC chemotherapeutic agent, in amounts that together are sufficient to treat
CC the patient. The method is useful for treating a patient having a
CC proliferative disease. The proliferative disease is cancer. A composition
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
CC human cancer cell in vivo or ex vivo, which involves contacting the cell
CC with the composition. The present sequence represents an antisense
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
CC sequence represents either T or U. There are multiple versions of this
CC sequence in the patent, the present sequence represents the sequence
CC shown in the main body of the specification.
XX
SQ Sequence 19 BP; 4 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGATATCTCCTTCAC 19
DB 1 GGATATCTCCTTCAC 14

RESULT 13
AEA09596
ID AEA09596 standard; DNA; 19 BP.
XX
XX AEA09596;
AC
XX
XX 14-JUL-2005 (first entry)
DT
XX

DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 107.
XX
XX Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH misc_difference 1..19
PT /tag= a
FT /note= "The residues represented by N are either T or U"

XX WO2005042030-A1.
PN
XX 12-MAY-2005.
PD
XX 29-OCT-2004; 2004WO-CA001900.
PF
XX 30-OCT-2003; 2003US-0516263P.
PR
XX (AEGE-) AEGERA THERAPEUTICS INC.
PA
XX Lacase E, Mcmanus D, Durkin JP;
PI
XX WPI; 2005-366517/37.
DR
XX
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
PT agent.
XX
XX Example 1; SEQ ID NO 107; 285pp; English.
PS
XX
XX The invention relates to a method of treating a patient having a
CC proliferative disease, comprising administering to the patient, an
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
CC chemotherapeutic agent, in amounts that together are sufficient to treat
CC the patient. The method is useful for treating a patient having a
CC proliferative disease. The proliferative disease is cancer. A composition
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
CC human cancer cell in vivo or ex vivo, which involves contacting the cell
CC with the composition. The present sequence represents an antisense
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
CC sequence represents either T or U. There are multiple versions of this
CC sequence in the patent, the present sequence represents the sequence
CC shown in the sequence listing.
XX
SQ Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;

Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTCAC 19
DB 1 CGCAGCGNANCCNNCAC 19

RESULT 14
AEC23674/C
ID AEC23674 standard; DNA; 19 BP.
XX
XX AEC23674;
AC
XX
XX 20-OCT-2005 (first entry)
DT
XX Forward primer for amplification of genomic CAPN1, seq id 10.
XX
XX Meat; animal breeding; SNP detection;
KM micromolar calcium activated neutral protease; mu-calpain; CAPN1; PCR;
KW primer; ss.
XX

OS Bos taurus.
 XX US2005181373-A1.
 XX
 XX 18-AUG-2005.
 PD
 XX 18-DEC-2003; 2003US-00739904.
 PF
 XX 18-DEC-2003; 2003US-00739904.
 PR
 XX 18-DEC-2003; 2003US-00739904.
 PA (SMIT/) SMITH T P.
 PA (CASA/) CASAS E.
 XX
 PI Smith TP, Casas E;
 XX WPI; 2005-554241/56.
 DR
 XX Determining one or more alleles of the gene encoding micromolar calcium
 PT activated neutral protease effecting meat tenderness by assaying a sample
 PT of nucleic acids from a bovine for the presence of single nucleotide
 PT polymorphisms.
 XX

Example 2; SEQ ID NO 10; 39pp; English.

XX The invention relates to a method for determining one or more alleles of
 CC the gene encoding micromolar calcium activated neutral protease effecting
 CC meat tenderness in a bovine animal. The method comprises assaying a
 CC sample of nucleic acids (genomic DNA, cDNA, or RNA) from a bovine for the
 CC presence of one or more single nucleotide polymorphisms in the bovine
 CC CAPN1 gene encoding micromolar calcium activated neutral protease (mu-
 CC calpain). In determining one or more alleles of the gene encoding
 CC micromolar calcium activated neutral protease effecting meat tenderness
 CC in a bovine animal, the single nucleotide polymorphisms correspond to
 CC position 18 of exon 9 of AEC23667, position 17 of exon 14 of AEC23668,
 CC and position 185 on Intron 19 of AEC23668. The method further comprises
 CC selecting those bovine for breeding where the polymorphism at position 18
 CC on exon 9 encodes alanine at amino acid 316 of the bovine micromolar
 CC calcium activated neutral protease. The method further comprises
 CC selecting those bovine for breeding where the polymorphism at position 17
 CC on exon 14 encodes valine at amino acid 530 of the bovine micromolar
 CC calcium activated neutral protease. The method further comprises
 CC selecting those bovine for breeding where the polymorphism at position
 CC 185 on Intron 19 comprises the presence of cytosine. In identifying one
 CC or more mutations in micromolar calcium activated neutral protease of
 CC bovine, the presence of alanine at amino acid 316, or valine at amino
 CC acid 539 of the bovine micromolar calcium activated neutral protease is
 CC indicative of increased meat tenderness. The method is useful for
 CC determining one or more alleles of the gene encoding micromolar calcium
 CC activated neutral protease effecting meat tenderness in a bovine animal.
 CC Sequences given in records for AEC23672-AEC23741 represent primers used
 CC in an example from the invention in the amplification of genomic CAPN1.
 CC
 XX

Sequence 19 BP; 6 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 68.4%; Score 13; DB 14; Length 19;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CACGGATCTCTCT 15
 |||||
 Db 17 CACGGATCTCTCT 5

RESULT 15
 AEA10089
 ID AEA10089 standard; DNA; 19 BP.
 XX
 AC AEA10089;
 XX
 DT 14-JUL-2005 (first entry)
 XX
 DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 110.
 XX

KW Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH modified_base 1..3
 FT modified_base 1..3
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER = 2'-O-methyl X RNA"
 FT modified_base 17..19
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER = 2'-O-methyl X RNA"
 FT
 EN W0205042030-A1.
 XX
 PD 12-MAY-2005.
 XX
 PD 29-OCT-2004; 2004WO-CAN001900.
 XX
 PF 29-OCT-2003; 2003US-0516263P.
 XX
 PR 30-OCT-2003; 2003US-0516263P.
 XX
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Lacasease E, Mcmannus D, Durkin JP;
 XX WPI; 2005-366517/37.
 DR

XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
 PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering
 PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
 PT agent.
 XX
 XX Example 1; SEQ ID NO 110; 285pp; English.
 PS
 XX The invention relates to a method of treating a patient having a
 CC proliferative disease, comprising administering to the patient, an
 CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
 CC chemotherapeutic agent, in amounts that together are sufficient to treat
 CC the patient. The method is useful for treating a patient having a
 CC proliferative disease. The proliferative disease is cancer. A composition
 CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
 CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
 CC human cancer cell in vivo or ex vivo, which involves contacting the cell
 CC with the composition. The present sequence represents an antisense
 CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
 CC sequence represents either T or U. There are multiple versions of this
 CC sequence in the patent, the present sequence represents the sequence
 CC shown in the main body of the specification.
 CC
 XX

Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 66.3%; Score 12.6; DB 14; Length 19;
 Best Local Similarity 78.9%; Pred. No. 1.3e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCACGGATCTCTCTCAC 19
 |||||
 Db 1 CGCACCGTATCTGTCTCAC 19

RESULT 16
 ADQ61052/C
 ID ADQ61052 standard; RNA; 19 BP.
 XX
 AC ADQ61052;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Anti-HCK siRNA related DNA sequence SEQ ID NO:754.
 XX
 KM se; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;

KW RNA interference.
 XX Synthetic.
 OS
 PN MO2004045543-A2.
 XX
 XX
 PD 03-JUN-2004.
 XX
 PF 14-NOV-2003; 2003WO-US036787.
 XX
 PR 14-NOV-2002; 2002US-0426137P.
 PR 10-SEP-2003; 2003US-0502050P.
 XX
 PA (DHAR-) DHARMACON INC.
 XX
 PI Anastasia K, Angela R, Devin L, William M, Stephen S;
 XX WPI; 2004-420527/39.
 DR
 XX
 XX
 PT Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
 PT by selecting a target gene and measuring the functionality of the
 PT nucleotide sequences that are complementary to a stretch of nucleotides
 PT of the target sequence.
 XX
 PS Example 12; SEQ ID NO 754; 199pp; English.
 XX
 XX The invention relates to a novel method for selecting siRNA (short
 CC interfering RNA) comprising selecting an siRNA molecule of 19-25
 CC nucleoside bases by selecting a target gene and measuring the
 CC functionality of sequences of 19-25 nucleotides in length that are
 CC substantially complementary to a stretch of nucleotides of the target
 CC sequence, where the functionality is dependent upon non-target specific
 CC criteria. Also claimed are methods for gene-silencing, developing an
 CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved
 CC functionality, selecting hyperfunctional siRNA, an siRNA molecule
 CC effective at silencing Bcl-2, and a kit for gene silencing comprising the
 CC siRNA. The siRNA molecule comprises a sequence substantially similar to a
 CC sequence consisting of GCGAGUAGUGAUGAAGU; GAAGACUUCUCUACGUUAG;
 CC GUACGACACCGGAGAAU; AGAUGAGUAGAUGAAGU; GAAGACUUCUCUACGUUAG;
 CC CAUGGCGCUCUGUUGA; UCGGCGCUCUGUUGA; GAGUAGUAGAAGUACA;
 CC GGAAGUAGUAGAAGUAC; and GAAGACUUCUCUACGUUAG. The siRNA molecule
 CC comprises a sense strand and an anti-sense strand. The siRNA molecule
 CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
 CC pairs. The kit comprises at least two siRNA, comprising a first optimised
 CC siRNA and a second optimised siRNA. The method is useful in selecting
 CC siRNA for generating a gene silencing reagent. The present invention is
 CC used in the exemplification of the invention. The sequence is shown in
 CC the specification as DNA, but described as siRNA.
 XX
 SQ Sequence 19 BP; 7 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 65.3%; Score 12.4; DB 12; Length 19;
 Best Local Similarity 92.9%; Pred. No. 1.6e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 CAGGATCTCTCTT 16
 Db 16 CAGGATCTCTCTT 3
 XX
 RESULT 17
 AAX24944
 ID AAX24944 standard; DNA; 19 BP.
 XX
 AC AAX24944;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 XX Mouse oestrogen receptor beta gene reverse primer 7.
 DE
 XX Oestrogen receptor; ER beta-3; ER beta-c; mouse; tumour; diagnosis;
 KM therapy; PCR; primer; ss.
 XX

OS Synthetic.
 OS Mus musculus.
 OS
 PN WO9905170-A1.
 XX
 XX
 PD 04-FEB-1999.
 XX
 PF 28-JUL-1998; 98WO-US015539.
 XX
 PR 28-JUL-1997; 97US-0053869P.
 PR 30-JUL-1997; 97US-0054210P.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI Denton R, Galien R, Rische-Rigon M, Fraasion C;
 XX WPI; 1999-142852/12.
 DR
 XX
 XX
 PT Human oestrogen receptor beta-3 - useful in treating and monitoring
 PT tumours.
 PT
 XX
 PS Example 1; Page 44; 89pp; English.
 XX
 XX This reverse primer is specific to the mouse oestrogen receptor beta (ER
 CC beta). It was used with an adaptor primer in the 5'RACE amplification of
 CC cDNA prepared from mouse ovary mRNA. Murine clone ovary beta-3 (see
 CC AAX24935) encoding the complete oestrogen receptor beta (ER beta-C, see
 CC AAW8128) was obtained. The invention provides methods for identifying
 CC agents that block or augment ER beta-c mediated transcriptional
 CC regulation, methods to determine whether ER beta-c or its isoforms is
 CC being expressed in tissues or cells, and methods of identifying and using
 CC agents that block the transcriptional regulation of genes by ER beta-c or
 CC its isoforms, which in turn modulates other biological and pathological
 CC processes
 XX
 SQ Sequence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 62.1%; Score 11.8; DB 2; Length 19;
 Best Local Similarity 86.7%; Pred. No. 3.4e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 CCGATCTCTCTTCTT 19
 Db 2 CAGTACTCTCTTCTT 16
 XX
 RESULT 18
 AAX33389
 ID AAX33389 standard; DNA; 19 BP.
 XX
 AC AAX33389;
 XX
 DT 25-JUN-1999 (first entry)
 XX
 XX Murine mER beta-3 PCR primer 7.
 DE
 XX Oestrogen receptor beta; oestrogen receptor beta; ER beta; PCR primer; ss.
 KM
 XX Synthetic.
 OS Mus sp.
 OS
 PN WO9905171-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 28-JUL-1998; 98WO-US015540.
 XX
 PR 28-JUL-1997; 97US-0053869P.
 PR 30-JUL-1997; 97US-0054210P.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI Baron R, Denton R, Chambon P, Dupont S, Garnier J;

XX WPI; 1999-142853/12.
 DR Novel murine oestrogen receptor-beta genes and splice variants - useful
 XX for treating oestrogen receptor-beta mediated disorders.
 PT
 XX Example 1; Page 43; 89pp; English.
 XX
 CC The present invention describes the murine complete oestrogen receptor
 CC beta (MER beta c; also designated MER beta-3). The present sequence
 CC represents a PCR primer used in the cloning of MER beta c. The protein
 CC can be used to screen for agents that modulate or block the interaction
 CC between the ER beta c protein and physiological, stilbene or
 CC triphenylethylene (anti)oestrogens. The antibody which binds the protein
 CC can be used in assays to detect activation of the ER beta protein and can
 CC be used for subcellular localisation of the protein. The complementary
 CC nucleic acid can be used to inhibit expression of the ER beta c nucleic
 CC acid
 XX
 SQ Sequence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 62.1%; Score 11.8; DB 2; Length 19;
 Best Local Similarity 86.7%; Pred. No. 3.4e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 5 CGGTATCTCCTTGAC 19
 Db 2 CAGTAGCTCTTCCAC 16
 RESULT 19
 AEF14562/c
 ID AEF14562 standard; DNA; 19 BP.
 AC AEF14562;
 XX
 DT 09-MAR-2006 (first entry)
 XX
 DE Human chondrocyte anabolic stimulation associated KD SEQ ID NO 279.
 XX
 KW Osteopathic; Nootropic; Neuroprotective; Dermatological;
 KM Antiinflammatory; Antiarthritic; Antiarthritic; musculoskeletal disease;
 KM chondrocyte anabolic stimulator; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2005124342-A2.
 XX
 PD 29-DEC-2005.
 XX
 PF 21-JUN-2005; 2005WO-EP052875.
 XX
 PR 21-JUN-2004; 2004US-0581568P.
 XX
 PA (GALA-) GALAPAGOS NV.
 XX
 PI Vandeghinste N, Tomme PHM, Michiels F, Ma L, Mille-Baker B;
 PI Van Es HMG;
 XX
 DR WPI; 2006-067565/07.
 XX
 PT Identifying a compound that induces chondrocyte anabolic stimulation,
 PT useful for treating osteoarthritis, comprises measuring a compound-
 PT polypeptide property related to the anabolic stimulation of chondrocytes.
 CC
 PS Claim 19; SEQ ID NO 279; 179pp; English.
 XX
 CC The invention relates to a method of identifying a compound that induces
 CC chondrocyte anabolic stimulation. The methods and agent are useful for
 CC treating and/or preventing a disease involving a systemic or local
 CC decrease in cartilage, e.g. osteoarthritis, rheumatoid arthritis,
 CC psoriatic arthritis, juvenile rheumatoid arthritis, gouty arthritis,
 CC septic or infectious arthritis, reactive arthritis, reflex sympathetic

CC dystrophy, algodystrophy, Tietze syndrome or costal chondritis.
 CC fibromyalgia, osteochondritis, neurogenic or neuropathic arthritis,
 CC arthropathy, osteoarthritis deformans endemica, Meulens disease,
 CC Handicod disease, degeneration resulting from fibromyalgia, systemic
 CC lupus erythematosus, scleroderma, ankylosing spondylitis, hereditary
 CC chondrolysis, chondrodysplasia, pseudochondrodysplasia, microtia,
 CC anotia, and metaphyseal chondrodysplasia. The agent is useful in the
 CC manufacture of a medicament for the treating and/or preventing a disease
 CC involving a decrease in mean cartilage thickness, e.g. osteoarthritis,
 CC hyperaldemia of malignancy, multiple myelomatosis, hyperparathyroidism,
 CC and hyperthyroidism. The present sequence represents a human chondrocyte
 CC anabolic stimulation associated KD target sequence.
 XX
 SQ Sequence 19 BP; 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 62.1%; Score 11.8; DB 15; Length 19;
 Best Local Similarity 86.7%; Pred. No. 3.4e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 5 CGGTATCTCCTTGAC 19
 Db 17 CAGTATCTCCTTGAC 3
 RESULT 20
 ADF73037
 ID ADF73037 standard; cDNA; 19 BP.
 AC ADF73037;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE DNA sequence of the invention #7.
 XX
 KW human repair gene DNA polymerase beta; gene therapy; esophagus cancer;
 KM es.
 XX
 OS Synthetic.
 XX
 PN CN1366047-A.
 XX
 PD 28-AUG-2002.
 XX
 PF 24-AUG-2001; 2001CN-00128374.
 XX
 PR 24-AUG-2001; 2001CN-00128374.
 XX
 PA (UYZH-) UNIV ZHENGZHOU.
 XX
 PI Dong Z, Zhao G, Zhao Q;
 XX
 DR WPI; 2003-240398/24.
 XX
 PT Human DNA polymerase beta mutant gene and its corresponding protein.
 PT
 XX
 PS Disclosure; SEQ ID NO 14; 18pp; Chinese.
 XX
 CC The present invention relates to a cDNA sequence of human repair gene DNA
 CC polymerase beta, which is a specific representation of DNA polymerase
 CC beta in esophagus cancer. The protein coded by it has fully lost the DNA
 CC repair activity of DNA polymerase beta. It can be used for early
 CC diagnosis and gene therapy of esophagus cancer. The present sequence is a
 CC DNA sequence of the invention.
 XX
 SQ Sequence 19 BP; 3 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 60.0%; Score 11.4; DB 10; Length 19;
 Best Local Similarity 92.3%; Pred. No. 5.5e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 6 GGATATCTCCTTCA 18
 Db 6 GGATCTCTCTTCA 18

```
RESULT 21
ACD28194
ID ACD28194 standard; DNA; 19 BP.
XX
XX
AC ACD28194;
XX
XX
DT 08-OCT-2003 (first entry)
XX
DE Human repair gene DNA polymerase beta related oligonucleotide #5.
XX
XX Human; repair gene; DNA polymerase beta; oesophagus cancer;
XX DNA repair activity; gene therapy; ss.
XX
OS Unidentified.
XX
XX CN1366047-A.
XX
XX 28-AUG-2002.
XX
XX 24-AUG-2001; 2001CN-00128374.
XX
XX 24-AUG-2001; 2001CN-00128374.
XX
XX (UYZH-) UNIV ZHENGZHOU.
XX
XX Dong Z, Zhao G, Zhao Q;
XX
XX WPI; 2003-240398/24.
XX
XX Human DNA polymerase beta mutant gene and its corresponding protein.
XX
XX Example 2; Page 9 (Disclosure); 11pp; Chinese.
XX
XX The present invention discloses a cDNA sequence of human repair gene DNA
XX polymerase beta, which is a specific representation of DNA polymerase
XX beta in oesophagus cancer. The protein coded by it has fully lost the DNA
XX repair activity of DNA polymerase beta. It can be used for early
XX diagnosis and gene therapy of esophagus cancer. This sequence represents
XX a human DNA polymerase beta associated oligonucleotide
XX
XX Sequence 19 BP; 3 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 11.4; DB 10; Length 19;
XX Best Local Similarity 92.3%; Pred. No. 5.5e+04;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 6 GGATCTCCTTCA 18
DB |||||
6 GGATCCTCCTTCA 18

RESULT 22
AAZ73203
ID AAZ73203 standard; DNA; 19 BP.
XX
XX AAZ73203;
XX
XX 10-SEP-2001 (first entry)
XX
XX Human biallelic marker upstream amplification primer SEQ ID NO:7559.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO954500-A2.
XX
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PD 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-1B000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GBST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX
XX Claim 9; Page 1842; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ6579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the invention
XX have a variety of uses: they can be used for high density mapping of the
XX human genome, and in complex association studies and haplotyping studies
XX which are useful in determining the genetic basis for disease states.
XX Compositions and methods of the invention can also be useful for the
XX identification of the targets for the development of pharmaceutical
XX agents and diagnostic methods, as well as the characterisation of the
XX differential efficacious responses to and side effects from
XX pharmaceutical agents acting on a disease as well as other treatment.
XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX 3367, are not actually given a sequence in the Sequence Listing from the
XX present invention
XX
XX Sequence 19 BP; 1 A; 6 C; 2 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 57.9%; Score 11; DB 3; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 8.8e+04;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 7 GATCTCCTTC 17
DB |||||
1 GATCTCCTTC 11

RESULT 23
AD061051/C
ID AD061051 standard; RNA; 19 BP.
XX
XX AD061051;
XX
XX 09-SEP-2004 (first entry)
XX
XX Anti-HCK siRNA related DNA sequence SEQ ID NO:753.
XX
XX ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
XX RNA interference.
XX
XX Synthetic.
XX
XX WO2004045543-A2.
XX
XX 03-JUN-2004.
XX
XX 14-NOV-2003; 2003WO-US036787.
XX
XX 14-NOV-2002; 2002US-0426137P.
XX
XX 10-SEP-2003; 2003US-0502050P.
XX
XX (DHAR-) DHARMACON INC.
XX
XX Anastasia K, Angela R, Devin L, William M, Stephen S;
XX
```

DR WPI; 2004-420527/39.
XX Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
PT by selecting a target gene and measuring the functionality of the
PT nucleotide sequences that are complementary to a stretch of nucleotides
PT of the target sequence.
XX
PS Example 12; SEQ ID NO 753; 199pp; English.
XX
CC The invention relates to a novel method for selecting siRNA (short
CC interfering RNA) comprising selecting an siRNA molecule of 19-25
CC nucleoside bases by selecting a target gene and measuring the
CC functionality of sequences of 19-25 nucleotides in length that are
CC substantially complementary to a stretch of nucleotides of the target
CC sequence, where the functionality is dependent upon non-target specific
CC criteria. Also claimed are methods for gene-silencing, developing an
CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved
CC functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC siRNA. The siRNA molecule comprises a sequence substantially similar to a
CC sequence consisting of GGAGAGUAGUAGAGUA; GAAGUACUCCUCCUCCU;
CC GUACGACACCGGAGAU; AGAUAGUAGUAGUAGAU; UGAAGUCCUCCUCCU;
CC CANGCGCCUCCUCCU; UCGGCGCCUCCUCCU; GAGAUAGUAGUAGUAGUA;
CC GGAGUAGUAGUAGUAGUA; and GAGACUCCUCCUCCU. The siRNA molecule
CC comprises a sense strand and an anti-sense strand. The siRNA molecule
CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
CC pairs. The kit comprises at least two siRNA, comprising a first optimised
CC siRNA and a second optimised siRNA. The method is useful in selecting
CC siRNA for generating a gene silencing reagent. The present sequence is
CC used in the exemplification of the invention. The sequence is shown in
CC the specification as DNA, but described as siRNA.
XX
SQ Sequence 19 BP; 8 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
XX
Query Match 57.9%; Score 11; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 3 CACGGTATCTC 13
Db 11 CACGGTATCTC 1
XX
RESULT 24
ADY83894
XX ADY83894 standard; DNA, 19 BP.
XX
AC ADY83894;
XX
DT 16-JUN-2005 (first entry)
XX
DE Escherichia coli gyrA gene microarray capture probe, E.coli_GYA87G5.
XX
KM quinolone; DNA microarray; probe; ss.
XX
OS Escherichia coli.
XX
OS Synthetic.
XX
PN US2005069897-A1.
XX
PD 31-MAR-2005.
XX
PF 29-SEP-2003; 2003US-00671883.
XX
PR 29-SEP-2003; 2003US-00671883.
XX
PA (EPPE-) EPPENDORF AG.
XX
PI Yu X, Susa M, Knabbe C, Schmidt R, Bachmann TT;
XX WPI; 2005-261625/27.
XX
XX Detecting quinolone resistant Escherichia coli strains in biological

PT sample by contacting DNA of sample with microarray having capture probes
PT derived from gyrA gene of E.coli, determining change in nucleic acid at
PT specific positions.
XX
PS Claim 8; SEQ ID NO 35; 20pp; English.
XX
CC The invention relates to a novel method for detecting quinolone resistant
CC Escherichia coli strains in a biological sample. The method involves
CC contacting sample DNA with a microarray having two sets of capture probes
CC and determining at which location on the array binding occurs, where a
CC change in a nucleic acid at one or more positions results in a change of
CC an amino acid and is indicative of a resistance against quinolones. The
CC invention further comprises: a microarray containing, at specific
CC predetermined locations of the array, two sets of capture probes derived
CC from the sequence of a gyrA gene of E. coli; and a kit for performing the
CC method, containing the microarray, and optionally buffers and reagents.
CC The method is useful for detecting the presence of quinolone resistant
CC Escherichia coli strains in a biological sample. This polynucleotide
CC sequence represents a possible capture probe of the E. coli gyrA gene for
CC use in the microarray of the invention.
XX
SQ Sequence 19 BP; 3 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 57.9%; Score 11; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 GCACGGTATCT 12
Db 5 GCACGGTATCT 15
XX
RESULT 25
ADY83902
XX ADY83902 standard; DNA, 19 BP.
XX
AC ADY83902;
XX
DT 16-JUN-2005 (first entry)
XX
DE Escherichia coli gyrA gene microarray capture probe, E.coli_GYA87G7.
XX
KM quinolone; DNA microarray; probe; ss.
XX
OS Escherichia coli.
XX
OS Synthetic.
XX
PN US2005069897-A1.
XX
PD 31-MAR-2005.
XX
PF 29-SEP-2003; 2003US-00671883.
XX
PR 29-SEP-2003; 2003US-00671883.
XX
PA (EPPE-) EPPENDORF AG.
XX
PI Yu X, Susa M, Knabbe C, Schmidt R, Bachmann TT;
XX WPI; 2005-261625/27.
XX
DR
XX
PT Detecting quinolone resistant Escherichia coli strains in biological
PT sample by contacting DNA of sample with microarray having capture probes
PT derived from gyrA gene of E.coli, determining change in nucleic acid at
PT specific positions.
XX
PS Claim 8; SEQ ID NO 43; 20pp; English.
XX
CC The invention relates to a novel method for detecting quinolone resistant
CC Escherichia coli strains in a biological sample. The method involves
CC contacting sample DNA with a microarray having two sets of capture probes
CC and determining at which location on the array binding occurs, where a
CC change in a nucleic acid at one or more positions results in a change of

CC an amino acid and is indicative of a resistance against quinolones. The
 CC invention further comprises: a microarray containing, at specific
 CC predetermined locations of the array, two sets of capture probes derived
 CC from the sequence of a gyrA gene of *E. coli*; and a kit for performing the
 CC method, containing the microarray, and optionally buffers and reagents.
 CC The method is useful for detecting the presence of quinolone resistant
 CC *Escherichia coli* strains in a biological sample. This polynucleotide
 CC sequence represents a possible capture probe of the *E. coli* gyrA gene for
 CC use in the microarray of the invention.

XX Sequence 19 BP; 3 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 57.9%; Score 11; DB 14; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCACGGTATCT 12
 Db 5 GCACGGTATCT 15

RESULT 26
 AEA02570/c
 ID AEA02570 standard; RNA; 19 BP.

AC AEA02570;
 XX
 DT 28-JUL-2005 (first entry)
 XX

DE Cholesteryl ester transfer protein siRNA SEQ ID NO 139.

XX short interfering RNA; siRNA; gene silencing; RNA interference;
 KW Respiratory-Gen.; Antiasthmatic; Antiallergic; Antiinflammatory;
 KW Neuroprotective; Nootropic; Uropathic;
 KW chronic obstructive pulmonary disease; asthma; allergic rhinitis;
 KW sinusitis; inflammation; allergy; cystic fibrosis; alzheimer's disease;
 KW mutation disorder; cholinergic receptor muscarinic 3; CHRM3; ss.

XX Synthetic.

XX WO2005045041-A2.

XX 19-MAY-2005.

PF 19-AUG-2004; 2004WO-US027404.

XX 23-OCT-2003; 2003US-00693059.

PR 24-NOV-2003; 2003US-00720448.

PR 03-DEC-2003; 2003US-00727780.

PR 14-JAN-2004; 2004US-00757803.

PR 10-FEB-2004; 2004US-0543480P.

PR 13-FEB-2004; 2004US-00780447.

PR 16-APR-2004; 2004US-00826966.

PR 30-APR-2004; 2004WO-US013456.

PR 24-MAY-2004; 2004WO-US016390.

PR 09-JUN-2004; 2004US-00864044.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Polisky B;

XX MPI; 2005-347065/35.

XX New short interfering nucleic acid molecule that directs cleavage of a
 PT cholesteryl ester transfer protein RNA, useful for treating or preventing
 PT hypercholesterolemia, hyperlipidemia, and/or cardiovascular disease.
 XX
 XX Claim 33; SEQ ID NO 139; 185bp; English.
 CC The invention relates to a chemically synthesized double stranded short
 CC interfering nucleic acid (siRNA) molecule that directs cleavage of a
 CC cholesteryl ester transfer protein (CETP) RNA via RNA interference
 CC (RNAi). The siRNA molecule, compounds, compositions, and methods are

CC useful for treating or preventing hypercholesterolemia, hyperlipidemia,
 CC and/or cardiovascular disease, e.g. coronary heart disease,
 CC cerebrovascular disease, aortic stenosis, peripheral vascular disease
 CC and/or atherosclerosis. The present sequence represents a cholesteryl
 CC ester transfer protein siRNA.

XX Sequence 19 BP; 8 A; 0 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 57.9%; Score 11; DB 14; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATCTCCTTCAC 19
 Db 14 ATCTCCTTCAC 4

RESULT 27
 AEA02470
 ID AEA02470 standard; RNA; 19 BP.

AC AEA02470;
 XX

DT 28-JUL-2005 (first entry)
 XX

DE Cholesteryl ester transfer protein siRNA SEQ ID NO 39.

XX short interfering RNA; siRNA; gene silencing; RNA interference;
 KW Respiratory-Gen.; Antiasthmatic; Antiallergic; Antiinflammatory;
 KW Neuroprotective; Nootropic; Uropathic;
 KW chronic obstructive pulmonary disease; asthma; allergic rhinitis;
 KW sinusitis; inflammation; allergy; cystic fibrosis; alzheimer's disease;
 KW mutation disorder; cholinergic receptor muscarinic 3; CHRM3; ss.

XX Synthetic.

XX WO2005045041-A2.

XX 19-MAY-2005.

PF 19-AUG-2004; 2004WO-US027404.

XX 23-OCT-2003; 2003US-00693059.

PR 24-NOV-2003; 2003US-00720448.

PR 03-DEC-2003; 2003US-00727780.

PR 14-JAN-2004; 2004US-00757803.

PR 10-FEB-2004; 2004US-0543480P.

PR 13-FEB-2004; 2004US-00780447.

PR 16-APR-2004; 2004US-00826966.

PR 30-APR-2004; 2004WO-US013456.

PR 24-MAY-2004; 2004WO-US016390.

PR 09-JUN-2004; 2004US-00864044.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Polisky B;

XX MPI; 2005-347065/35.

XX New short interfering nucleic acid molecule that directs cleavage of a
 PT cholesteryl ester transfer protein RNA, useful for treating or preventing
 PT hypercholesterolemia, hyperlipidemia, and/or cardiovascular disease.
 XX
 XX Claim 33; SEQ ID NO 39; 185bp; English.
 CC The invention relates to a chemically synthesized double stranded short
 CC interfering nucleic acid (siRNA) molecule that directs cleavage of a
 CC cholesteryl ester transfer protein (CETP) RNA via RNA interference
 CC (RNAi). The siRNA molecule, compounds, compositions, and methods are
 CC useful for treating or preventing hypercholesterolemia, hyperlipidemia,
 CC and/or cardiovascular disease, e.g. coronary heart disease,
 CC cerebrovascular disease, aortic stenosis, peripheral vascular disease
 CC and/or atherosclerosis. The present sequence represents a cholesteryl

CC ester transfer protein siRNA.

XX Sequence 19 BP; 3 A; 8 C; 0 G; 0 T; 8 U; 0 Other;

Query Match 57.9%; Score 11; DB 14; Length 19;

Best Local Similarity 63.6%; Pred. No. 8.8e+04; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

9 ATCTGCTTAC 19

6 AUCUCCUCCAC 16

RESULT 28

ABE43434 ID ABE43434 standard; CDNA; 19 BP.

AC ABE43434;

DT 09-FEB-2006 (first entry)

DE Human hairless homolog CDNA 19-mer fragment SEQ ID NO 2570.

KM ss; hirsutism; depilatory; hairless homolog.

OS Homo sapiens.

PN WO2005105157-A2.

PD 10-NOV-2005.

PF 22-APR-2005; 2005WO-US013770.

PR 23-APR-2004; 2004US-0565127P.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Cristiano AM;

XX WPI; 2005-769492/78.

XX Removing human hair comprises applying to a human in an area comprising hair follicles a double stranded nucleic acid molecule comprising a sequence of at least a portion of human hairless protein mRNA.

PS Disclosure; SEQ ID NO 2570; 216bp; English.

CC The invention relates to a method of human hair removal which comprises applying to a human in an area comprising hair follicles a double stranded nucleic acid molecule comprising a sequence of at least a portion of human hairless protein mRNA or its complement. In the method of human hair removal, inhibition of hair growth in the area persists at least one month. The method comprises synchronizing hair growth cycles for hair follicles in the area. The method alternatively comprises contacting hair follicles in the region with a composition comprising at least one double stranded nucleic acid molecule able to inhibit hairless mRNA translation. The mammal is a human, mouse, rat, or bovine. The method, nucleic acid molecules and compositions useful for removing undesirable hair e.g. hirsutism. The present sequence represents a human hairless homolog CDNA 19-mer fragment.

XX Sequence 19 BP; 0 A; 11 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 57.9%; Score 11; DB 14; Length 19;

Best Local Similarity 73.7%; Pred. No. 8.8e+04; Mismatches 5; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 CGCAGGATCTCTTCCAC 19

1 CGCTCGCGCTCTCTTCCC 19

RESULT 29

ABE43433/C ID ABE43433 standard; CDNA; 19 BP.

AC ABE43433;

DT 09-FEB-2006 (first entry)

DE Human hairless homolog CDNA 19-mer fragment SEQ ID NO 2569.

KM ss; hirsutism; depilatory; hairless homolog.

OS Homo sapiens.

PN WO2005105157-A2.

PD 10-NOV-2005.

PF 22-APR-2005; 2005WO-US013770.

PR 23-APR-2004; 2004US-0565127P.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Cristiano AM;

XX WPI; 2005-769492/78.

XX Removing human hair comprises applying to a human in an area comprising hair follicles a double stranded nucleic acid molecule comprising a sequence of at least a portion of human hairless protein mRNA.

PS Disclosure; SEQ ID NO 2569; 216bp; English.

CC The invention relates to a method of human hair removal which comprises applying to a human in an area comprising hair follicles a double stranded nucleic acid molecule comprising a sequence of at least a portion of human hairless protein mRNA or its complement. In the method of human hair removal, inhibition of hair growth in the area persists at least one month. The method comprises synchronizing hair growth cycles for hair follicles in the area. The method alternatively comprises contacting hair follicles in the region with a composition comprising at least one double stranded nucleic acid molecule able to inhibit hairless mRNA translation. The mammal is a human, mouse, rat, or bovine. The method, nucleic acid molecules and compositions useful for removing undesirable hair e.g. hirsutism. The present sequence represents a human hairless homolog CDNA 19-mer fragment.

XX Sequence 19 BP; 5 A; 3 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 57.9%; Score 11; DB 14; Length 19;

Best Local Similarity 73.7%; Pred. No. 8.8e+04; Mismatches 5; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 CGCAGGATCTCTTCCAC 19

19 CGCTCGCGCTCTCTTCCC 1

RESULT 30

AAA85544 ID AAA85544 standard; DNA; 19 BP.

AC AAA85544;

DT 04-DEC-2000 (first entry)

DE Cyclin A1 ribozyme binding site #166.

KM Ribozyme; hairpin; hammerhead; gene therapy; vasodilator; restenosis; ss.

OS Mammalia.

PN WO200032765-A2.

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XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 94; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AA82415 to AA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 4 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 56.8%; Score 10.8; DB 3; Length 19;
XX Best Local Similarity 85.7%; Pred. No. 1.1e+05;
XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 5 CGGTATCTCCTTCA 18
XX | | | | | | | |
XX 4 CAGTTTCCTCTTCA 17
XX
XX RESULT 31
XX AA85545
XX ID AA85545 standard; DNA; 19 BP.
XX
XX AAA85545;
XX
XX 04-DEC-2000 (first entry)
XX
XX Cyclin A1 ribozyme binding site #167.
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
XX Mammalia.
XX
XX WO200032765-A2.
XX
XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 94; 109pp; English.
XX
```

```
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
CC
CC Sequence 19 BP; 3 A; 7 C; 2 G; 7 T; 0 U; 0 Other;
CC
CC Query Match 56.8%; Score 10.8; DB 3; Length 19;
CC Best Local Similarity 85.7%; Pred. No. 1.1e+05;
CC Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CC
CC 5 CGGTATCTCCTTCA 18
CC | | | | | | | |
CC 2 CAGTTTCCTCTTCA 15
CC
CC RESULT 32
CC AA85542
CC ID AA85542 standard; DNA; 19 BP.
CC
CC AAA85542;
CC
CC 04-DEC-2000 (first entry)
CC
CC Cyclin A1 ribozyme binding site #164.
CC
CC Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
CC
CC Mammalia.
CC
CC WO200032765-A2.
CC
CC 08-JUN-2000.
CC
CC 06-DEC-1999; 99WO-US028772.
CC
CC 04-DEC-1998; 98US-0110954P.
CC
CC (IMMU-) IMMUSOL INC.
CC
CC Tritz R, Welch PJ, Barber JR, Robbins JM;
CC
CC WPI; 2000-412314/35.
CC
CC New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
CC RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
CC PCNA and Cyclin B1.
CC
CC Disclosure; Page 94; 109pp; English.
CC
```

```
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AA82415 to AA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 4 A; 8 C; 1 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 56.8%; Score 10.8; DB 3; Length 19;
XX Best Local Similarity 85.7%; Pred. No. 1.1e+05;
XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 5 CGGTATCTCCTTCA 18
XX | | | | | | | |
XX 6 CAGTTTCCTCTTCA 19
XX
```

```

RESULT 33
AA85543
ID AA85543 standard; DNA; 19 BP.
XX
AC AA85543;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cyclin A1 ribozyme binding site #165.
XX
KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tiltz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 94; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 56.8%; Score 10.8; DB 3; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCA 18
   |||||
Db 5 CAGTTCTCCTTCA 18

RESULT 34
AA85448/C
ID AA85448 standard; DNA; 19 BP.
XX
AC AA85448;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cyclin A1 ribozyme binding site #70.
XX
KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.

```

```

PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tiltz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 92; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 56.8%; Score 10.8; DB 3; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCA 18
   |||||
Db 17 CGGTGTCCTACTTCA 4

RESULT 35
AAC59851
ID AAC59851 standard; DNA; 19 BP.
XX
AC AAC59851;
XX
DT 26-JAN-2001 (first entry)
XX
DE Oligonucleotide probe for human DNA clone vpl6 1.
XX
KM Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
KM systemic lupus erythematosus; rheumatoid arthritis; anemia; stroke;
KM haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;
KM Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
KM contraceptive; infection; growth inhibition; hyperproliferative disorder;
KM psoriasis; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200055375-A1.
XX
PD 21-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US007285.
XX
PR 17-MAR-1999; 99US-0124808P.
PR 17-MAR-1999; 99US-0124916P.
PR 17-AUG-1999; 99US-0149639P.
PR 01-OCT-1999; 99US-0157247P.
PR 29-NOV-1999; 99US-0167824P.
PR 15-FEB-2000; 2000US-0182711P.
XX
PA (ALPH-) ALPHAGEN INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-638211/61.

```

XX Novel proteins and polypeptides useful for the treatment of e.g multiple
 PT sclerosis, systemic lupus erythematosus, rheumatoid arthritis, cancer,
 PT Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.
 XX
 PS Disclosure, Page 465; 493pp; English.

XX This invention relates to 59 human secreted proteins and the nucleotide
 CC sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745
 CC represent the proteins and their encoding nucleotide sequences, and
 CC sequences AAB34746-B34771 represent fragments of the proteins. Probes for
 CC the DNA sequences are represented by sequences AAC59847-C59956. The
 CC proteins exhibit neuroprotective, dermatological, immunosuppressive,
 CC antiinflammatory, antianaemic, nootropic, antiparkinsonian,
 CC cerebroprotective, haemostatic, vulnereary, cytostatic, antipsoriatic,
 CC antibacterial, vitucide, and fungicide activity. The proteins and
 CC nucleotide sequences are useful as nutritional sources or supplements and
 CC in research. The proteins are useful for treating immune deficiency and
 CC disorders, which may be genetic or resulting from infections, autoimmune
 CC disorders, such as multiple sclerosis, systemic lupus erythematosus,
 CC rheumatoid arthritis, and for treating myeloid or lymphoid cell
 CC deficiencies such as anaemias by regulating haematopoiesis. The proteins
 CC are also useful in compositions for bone, cartilage, tendon, ligament
 CC and/or nerve tissue growth or regeneration, for wound healing, tissue
 CC repair and replacement and in the treatment of wounds, incisions and
 CC ulcers. Other uses include in the treatment of central and peripheral
 CC nervous system and neuropathies such as Alzheimer's and Parkinson's
 CC diseases and Shy-Drager syndrome, and mechanical and traumatic disorders,
 CC such as spinal cord disorders, head trauma and stroke. The proteins may
 CC also be used as a contraceptive, and for treating coagulation disorders
 CC such as haemophilias. The protein and nucleotide sequences with cadherin
 CC activity are useful for treating cancer. Other uses for the protein
 CC include for inhibiting the growth, infection or function of, or killing,
 CC infectious agents such as bacteria, virus, fungi and other parasites, for
 CC effecting bodily characteristics such as height, weight, hair colour,
 CC effecting biophysics or cardiac cycles or rhythms, effecting metabolism,
 CC catabolism, anabolism, processing, utilization, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors,
 CC effecting behavioural characteristics, providing analgesic effects and
 CC for treating hyperproliferative disorders such as psoriasis

XX Sequence 19 BP; 2 A; 4 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 56.8%; Score 10.8; DB 3; Length 19;

Best Local Similarity 85.7%; Pred. No. 1.1e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCT 15
 |||||
 DB 4 GCAGGGTGTCTCT 17

RESULT 36

AAH60704

ID AAH60704 standard; DNA; 19 BP.

AC AAH60704;

DT 10-SEP-2001 (first entry)

XX Cyclin A1 ribozyme binding site SEQ ID NO:3128.

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnereary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; anti-seborrheic; antidiabetic; vitucide;
 KW antiskinking; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.

OS Homo sapiens.
 OS Synthetic.

XX WO20010362-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000MO-US029500.

XX 26-OCT-1999; 99US-0161532P.

XX (IMMU-) IMMUSOL INC.

XX Robbins JM, Tritel R;

XX WPI, 2001-300427/31.

XX Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependant kinases.

XX Example 1; Page 299; 408pp; English.

XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have anti-seborrheic,
 CC dermatological, cytostatic, anti-seborrheic, antidiabetic, antiskinking,
 CC ophthalmological, vulnereary, keratolytic and vitucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (II) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH5757 to AAH6209 represent sequences used in the
 CC exemplification of the present invention

XX Sequence 19 BP; 4 A; 8 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 56.8%; Score 10.8; DB 5; Length 19;

Best Local Similarity 85.7%; Pred. No. 1.1e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGTATCTCTCTCA 18
 |||||
 DB 6 CAGTTTCTCTTCA 19

RESULT 37

AAH60705

ID AAH60705 standard; DNA; 19 BP.

AC AAH60705;

DT 10-SEP-2001 (first entry)

XX Cyclin A1 ribozyme binding site SEQ ID NO:3129.

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnereary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; anti-seborrheic; antidiabetic; vitucide;
 KW antiskinking; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;

CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have anti-psoriasis,
CC dermatological, cytostatic, anti-seborrheic, anti-diabetic, anti-sclerotic,
CC ophthalmological, vascular, keratolytic and anticancer activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

RESULT 38	
AAH60706	
ID	AAH60706 standard; DNA; 19 BP.
ID	
AC	AAH60706;
XX	
DT	10-SEP-2001 (first entry)
XX	
XE	Cyclin A1 ribozyme binding site SEQ ID NO:3130

KM human, ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KM recombinant alic; target; ribozyme binding site; eye disease; vulnerability;
KM proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KM cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KM matrix metalloproteinase; growth factor; reductase; scarring; cytoskeletal
KM antiporatic; dermatological; antiseborrheic; antiadipetic; vitinide;
KM antisticking; ophthalmological; keratolytic; gene therapy; viral wart;

PS Example 1.; Page 299; 408bp; English.

```

RESULT 39
AAH60610/c
ID AAH60610 standard; DNA; 19 BP.
XX
XX
AC AAH60610;
XX
TT 10-SEP-2001 (first entry)
XX

```

XX Human; ribozyme therapy; hammerhead ribozyme;
KM recognition site; target; ribozyme binding site; eye disease; vulnery;
KM proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KM cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KM matrix metalloproteinase; growth factor; reductase; scarring; cytostatic

KM antipsoarctic; dermatological; antiseborrheic; antidiabetic; virucide;
 KM antisticking; ophthalmological; keratolytic; gene therapy; viral wart;
 KM atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KM basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KM sickle cell retinopathy; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 WO200130362-A2.
 PN
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-US029500.
 XX
 PR 26-OCT-1999; 99US-0161532P.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Robbins JM, Tritz R;
 XX
 DR WPI; 2001-300427/31.
 XX
 PT Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX
 SS Example 1; Page 292; 408bp; English.

CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have anti-proliferative,
CC dermatological, cytostatic, anti-neoplastic, anti-diabetic, anti-sclerotic,
CC ophthalmological, vulnary, keratolytic and antiviral activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
CC
CC Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
CC XX

Query Match	56.8%	Score 10.8	DB 5	Length 19
Best Local Similarity	85.7%	Pred. No. 1.1e+05		
Matches 12	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	5	CGGATCTCCTTCA	18	
db	17	CGGATCTACTTCA	4	

	RESULT	40
AAH60707		
ID	AAH60707	standard; DNA, 19 BP.
XX		
AC	AAH60707;	
XX		
DT	10-SEP-2001	(first entry)
XX		
DE	Cyclin A1 ribozyme binding site	SEQ ID NO:3131.
XX		
KW	Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerrary; proliferative disease; skin disease; psoriasis; diabetic retinopathy;	

KW	cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW	matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW	antiproliferative; dermatological; antiseborrheic; antidiabetic; vitamin D;
KW	antischistosomal; ophthalmological; keratolytic; gene therapy; viral wart;
KW	atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW	basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW	sickle cell retinopathy; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200130362-A2.
PD	
PD	03-MAY-2001.
XX	
PP	26-OCT-2000; 2000WO-US029500.
XX	
PR	26-OCT-1999; 99US-0161532P.
XX	
PA	(IMMU-) IMMUSOL INC.
XX	
PI	Robbins JM, Tritz R;
XX	
DR	WPI; 2001-300427/31.
XX	
PT	Treating proliferative skin or eye diseases and scarring, using ribozymes
PT	that cleave RNA encoding cytokines involved in inflammation, matrix
PT	metalloproteinases, growth factors and cell-cycle dependent kinases.

Example 1; Page 299; 408bp; English.

	Sequence	19 BP	3 A	7 C	2 G	7 T	0 U	0 Other
Query	Match	56.8%	Score 10.6	DB 5	Length 19			
	Best Local Similarity	85.7%	Pred. No. 1.1e+05					
Matches	12; Conservative	0	Mismatches 2	Indels 0	Gaps 0			
Qy	5 CGGATCTCCTTCA	18						
Db	2 CAGTTTCTCCTTCA	15						

Search completed: August 10, 2006, 08:56:12
Job time : 309.667 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 08:37:42 ; Search time 981.667 Seconds
(without alignments)
1237.692 Million cell updates/sec

Title: US-10-636-065-29
Perfect score: 19
Sequence: 1 cgcacgcatccttcac 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 141404

Minimum DB seq length: 19
Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl:.*
1: gb_env:.*
2: gb_pat:.*
3: gb_ph:.*
4: gb_pl:.*
5: gb_pr:.*
6: gb_ro:.*
7: gb_rts:.*
8: gb_ey:.*
9: gb_un:.*
10: gb_vi:.*
11: gb_ov:.*
12: gb_htg:.*
13: gb_in:.*
14: gb_om:.*
15: gb_ba:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	19	100.0	19	2	AR451384	AR451384 Sequence
2	19	100.0	19	2	AX411929	AX411929 Sequence
3	15	78.9	19	2	CS027764	CS027764 Sequence
4	15	78.9	19	2	CS028231	CS028231 Sequence
5	14	73.7	19	2	AX923594	AX923594 Sequence
6	14	73.7	19	2	AX923672	AX923672 Sequence
7	11.8	62.1	19	2	BD080793	BD080793 Human est
8	11.8	62.1	19	2	BD080808	BD080808 Novel est
9	11.8	62.1	19	2	CS251594	CS251594 Sequence
10	11	57.9	19	2	CS094047	CS094047 Sequence
11	11	57.9	19	2	CS094147	CS094147 Sequence
12	11	57.9	19	2	AR295824	AR295824 Sequence
13	10.8	56.8	19	2	AR573706	AR573706 Sequence
14	10.8	56.8	19	2	AR573800	AR573800 Sequence
15	10.8	56.8	19	2	AR573801	AR573801 Sequence
16	10.8	56.8	19	2	AR573802	AR573802 Sequence
17	10.8	56.8	19	2	AR573803	AR573803 Sequence
18	10.8	56.8	19	2	AX131816	AX131816 Sequence

19	10.8	56.8	19	2	AX131910	AX131910 Sequence
20	10.8	56.8	19	2	AX131911	AX131911 Sequence
21	10.8	56.8	19	2	AX131912	AX131912 Sequence
22	10.8	56.8	19	2	AX131913	AX131913 Sequence
23	10.6	55.8	19	2	CQ824220	CQ824220 Sequence
24	10.6	55.8	19	2	CS171759	CS171759 Sequence
25	10.6	55.8	19	2	ES4494	ES4494 Heat-resist
26	10.6	55.8	19	2	AR297589	AR297589 Sequence
27	10.6	55.8	19	2	AX117403	AX117403 Sequence
28	10.6	55.8	19	2	AX751584	AX751584 Sequence
29	10.6	55.8	19	2	AX837880	AX837880 Sequence
30	10.4	54.7	19	2	CS246174	CS246174 Sequence
31	10.4	54.7	19	2	AR293205	AR293205 Sequence
32	10.4	54.7	19	2	AR294484	AR294484 Sequence
33	10.4	54.7	19	2	AR533333	AR533333 Sequence
34	10.4	54.7	19	2	AR573804	AR573804 Sequence
35	10.4	54.7	19	2	AX131914	AX131914 Sequence
36	10.2	53.7	19	2	BD244859	BD244859 Oligonuc
37	10.2	53.7	19	2	CS128821	CS128821 Sequence
38	10.2	53.7	19	2	CS132095	CS132095 Sequence
39	10.2	53.7	19	2	CS197806	CS197806 Sequence
40	10.2	53.7	19	2	CS197807	CS197807 Sequence
41	10.2	53.7	19	2	CS197808	CS197808 Sequence
42	10.2	53.7	19	2	CS197809	CS197809 Sequence
43	10.2	53.7	19	2	CS197810	CS197810 Sequence
44	10.2	53.7	19	2	CS199558	CS199558 Sequence
45	10.2	53.7	19	2	CS199559	CS199559 Sequence
46	10.2	53.7	19	2	CS199560	CS199560 Sequence
47	10.2	53.7	19	2	CS199561	CS199561 Sequence
48	10.2	53.7	19	2	CS199562	CS199562 Sequence
49	10.2	53.7	19	2	AX378611	AX378611 Sequence
50	10.2	52.6	19	2	AR070723	AR070723 Sequence
51	10	52.6	19	2	BD000812	BD000812 Methods a
52	10	52.6	19	2	BD105849	BD105849 Novel ant
53	10	52.6	19	2	CS189923	CS189923 Sequence
54	10	52.6	19	2	CS193344	CS193344 Sequence
55	10	52.6	19	2	CS231374	CS231374 Sequence
56	10	52.6	19	2	CS248893	CS248893 Sequence
57	10	52.6	19	2	DD201537	DD201537 RNA Inter
58	10	52.6	19	2	DD201964	DD201964 RNA Inter
59	10	52.6	19	2	117109	117109 Sequence 2
60	10	52.6	19	2	162398	162398 Sequence 2
61	10	52.6	19	2	AR481863	AR481863 Sequence
62	10	52.6	19	2	AX769415	AX769415 Sequence
63	9.8	51.6	19	2	A98471	A98471 Sequence 10
64	9.8	51.6	19	2	AR067391	AR067391 Sequence
65	9.8	51.6	19	2	AR080800	AR080800 Sequence
66	9.8	51.6	19	2	AR160473	AR160473 Sequence
67	9.8	51.6	19	2	AR164071	AR164071 Sequence
68	9.8	51.6	19	2	BD015691	BD015691 Novel pro
69	9.8	51.6	19	2	BD015692	BD015692 Novel pro
70	9.8	51.6	19	2	BD094844	BD094844 Novel pro
71	9.8	51.6	19	2	BD094845	BD094845 Novel pro
72	9.8	51.6	19	2	BD124109	BD124109 Novel GAB
73	9.8	51.6	19	2	BD266184	BD266184 Universal
74	9.8	51.6	19	2	CQ988169	CQ988169 Sequence
75	9.8	51.6	19	2	CQ988252	CQ988252 Sequence
76	9.8	51.6	19	2	CS094102	CS094102 Sequence
77	9.8	51.6	19	2	CS094202	CS094202 Sequence
78	9.8	51.6	19	2	DD202532	DD202532 RNA Inter
79	9.8	51.6	19	2	DD202856	DD202856 RNA Inter
80	9.8	51.6	19	2	AR294258	AR294258 Sequence
81	9.8	51.6	19	2	AR631270	AR631270 Sequence
82	9.8	51.6	19	2	AR631271	AR631271 Sequence
83	9.8	51.6	19	2	AX054675	AX054675 Sequence
84	9.8	51.6	19	8	AB213933	AB213933 Synthetic
85	9.6	50.5	19	2	AX956573	AX956573 Sequence
86	9.6	50.5	19	2	BD195704	BD195704 In vivo u
87	9.6	50.5	19	2	BD243891	BD243891 STE20-rel
88	9.6	50.5	19	2	CQ776074	CQ776074 Sequence
89	9.6	50.5	19	2	CQ779515	CQ779515 Sequence
90	9.6	50.5	19	2	CQ965695	CQ965695 Sequence
91	9.6	50.5	19	2	CQ965800	CQ965800 Sequence

C 92	9.6	50.5	19	2	CS200808	Sequence	C 165	9.2	48.4	19	2	CS246098	Sequence
C 93	9.6	50.5	19	2	CS251845	Sequence	C 166	9.2	48.4	19	2	CS256216	Sequence
C 94	9.6	50.5	19	2	DD162073	Transgent	C 167	9.2	48.4	19	2	DD193039	Sequence
C 95	9.6	50.5	19	2	E33605	Novel proka	C 168	9.2	48.4	19	2	DD199036	RNA Inter
C 96	9.6	50.5	19	2	AR282797	Sequence	C 169	9.2	48.4	19	2	DD199361	RNA Inter
C 97	9.6	50.5	19	2	AR295377	Sequence	C 170	9.2	48.4	19	2	DD201552	RNA Inter
C 98	9.6	50.5	19	2	AR435644	Sequence	C 171	9.2	48.4	19	2	DD201552	RNA Inter
C 99	9.6	50.5	19	2	AR453245	Sequence	C 172	9.2	48.4	19	2	DD201979	RNA Inter
C 100	9.6	50.5	19	2	AR569954	Sequence	C 173	9.2	48.4	19	2	E30141	Method for
C 101	9.6	50.5	19	2	AR569954	Sequence	C 174	9.2	48.4	19	2	AR203016	Sequence
C 102	9.6	50.5	19	2	AX378467	Sequence	C 175	9.2	48.4	19	2	AR293419	Sequence
C 103	9.4	49.5	19	2	AX676163	Sequence	C 176	9.2	48.4	19	2	AR353644	Sequence
C 104	9.4	49.5	19	2	BD061246	A method	C 177	9.2	48.4	19	2	AR363491	Sequence
C 105	9.4	49.5	19	2	CQ902499	Sequence	C 178	9.2	48.4	19	2	AR365227	Sequence
C 106	9.4	49.5	19	2	CQ902510	Sequence	C 179	9.2	48.4	19	2	AR571809	Sequence
C 107	9.4	49.5	19	2	CQ902523	Sequence	C 180	9.2	48.4	19	2	AR571810	Sequence
C 108	9.4	49.5	19	2	CQ902524	Sequence	C 181	9.2	48.4	19	2	AR572101	Sequence
C 109	9.4	49.5	19	2	CQ902531	Sequence	C 182	9.2	48.4	19	2	AR572102	Sequence
C 110	9.4	49.5	19	2	CQ902542	Sequence	C 183	9.2	48.4	19	2	AX129919	Sequence
C 111	9.4	49.5	19	2	CQ902553	Sequence	C 184	9.2	48.4	19	2	AX129920	Sequence
C 112	9.4	49.5	19	2	CQ902564	Sequence	C 185	9.2	48.4	19	2	AX130211	Sequence
C 113	9.4	49.5	19	2	CQ902575	Sequence	C 186	9.2	48.4	19	2	AX130212	Sequence
C 114	9.4	49.5	19	2	CQ902586	Sequence	C 187	9.2	48.4	19	2	AX298518	Sequence
C 115	9.4	49.5	19	2	CQ902597	Sequence	C 188	9.2	48.4	19	2	AX302081	Sequence
C 116	9.4	49.5	19	2	CQ988227	Sequence	C 189	9.2	47.4	19	2	A49480	Sequence
C 117	9.4	49.5	19	2	CQ988310	Sequence	C 190	9.2	47.4	19	2	A50818	Sequence
C 118	9.4	49.5	19	2	CS052710	Sequence	C 191	9.2	47.4	19	2	AR079665	Sequence
C 119	9.4	49.5	19	2	CS092098	Sequence	C 192	9.2	47.4	19	2	AR125649	Sequence
C 120	9.4	49.5	19	2	CS096531	Sequence	C 193	9.2	47.4	19	2	AR233594	Sequence
C 121	9.4	49.5	19	2	CS096618	Sequence	C 194	9.2	47.4	19	2	AX923708	Sequence
C 122	9.4	49.5	19	2	CS223422	Sequence	C 195	9.2	47.4	19	2	AX923854	Sequence
C 123	9.4	49.5	19	2	CS231378	Sequence	C 196	9.2	47.4	19	2	BD087967	A method
C 124	9.4	49.5	19	2	CS231396	Sequence	C 197	9.2	47.4	19	2	BD174508	Method fo
C 125	9.4	49.5	19	2	DD202505	RNA Inter	C 198	9.2	47.4	19	2	BD186492	Method of
C 126	9.4	49.5	19	2	DD202829	RNA Inter	C 199	9.2	47.4	19	2	BD196939	Prostatic
C 127	9.4	49.5	19	2	AK573805	Sequence	C 200	9.2	47.4	19	2	CQ759039	Sequence
C 128	9.4	49.5	19	2	AK765023	Sequence	C 201	9.2	47.4	19	2	CQ801708	Sequence
C 129	9.4	49.5	19	2	AX131915	Sequence	C 202	9.2	47.4	19	2	CQ801954	Sequence
C 130	9.2	48.4	19	2	BD226459	Method an	C 203	9.2	47.4	19	2	CQ961212	Sequence
C 131	9.2	48.4	19	2	BD236470	Method an	C 204	9.2	47.4	19	2	CQ962863	Sequence
C 132	9.2	48.4	19	2	CQ786254	Sequence	C 205	9.2	47.4	19	2	CQ966178	Sequence
C 133	9.2	48.4	19	2	CQ799886	Sequence	C 206	9.2	47.4	19	2	CQ966206	Sequence
C 134	9.2	48.4	19	2	CQ961307	Sequence	C 207	9.2	47.4	19	2	CQ966387	Sequence
C 135	9.2	48.4	19	2	CQ962958	Sequence	C 208	9.2	47.4	19	2	CQ966415	Sequence
C 136	9.2	48.4	19	2	CQ987750	Sequence	C 209	9.2	47.4	19	2	CQ988332	Sequence
C 137	9.2	48.4	19	2	CQ988075	Sequence	C 210	9.2	47.4	19	2	CQ988456	Sequence
C 138	9.2	48.4	19	2	CQ988158	Sequence	C 211	9.2	47.4	19	2	CS089765	Sequence
C 139	9.2	48.4	19	2	CQ988241	Sequence	C 212	9.2	47.4	19	2	CS089769	Sequence
C 140	9.2	48.4	19	2	CS013271	Sequence	C 213	9.2	47.4	19	2	CS089772	Sequence
C 141	9.2	48.4	19	2	CS014598	Sequence	C 214	9.2	47.4	19	2	CS089927	Sequence
C 142	9.2	48.4	19	2	CS015012	Sequence	C 215	9.2	47.4	19	2	CS090461	Sequence
C 143	9.2	48.4	19	2	CS050332	Sequence	C 216	9.2	47.4	19	2	CS090465	Sequence
C 144	9.2	48.4	19	2	CS093150	Sequence	C 217	9.2	47.4	19	2	CS090468	Sequence
C 145	9.2	48.4	19	2	CS093457	Sequence	C 218	9.2	47.4	19	2	CS090623	Sequence
C 146	9.2	48.4	19	2	CS102052	Sequence	C 219	9.2	47.4	19	2	CS101722	Sequence
C 147	9.2	48.4	19	2	CS102189	Sequence	C 220	9.2	47.4	19	2	CS101845	Sequence
C 148	9.2	48.4	19	2	CS197448	Sequence	C 221	9.2	47.4	19	2	CS129011	Sequence
C 149	9.2	48.4	19	2	CS197449	Sequence	C 222	9.2	47.4	19	2	CS132280	Sequence
C 150	9.2	48.4	19	2	CS197450	Sequence	C 223	9.2	47.4	19	2	CS132418	Sequence
C 151	9.2	48.4	19	2	CS197451	Sequence	C 224	9.2	47.4	19	2	CS197912	Sequence
C 152	9.2	48.4	19	2	CS197452	Sequence	C 225	9.2	47.4	19	2	CS197913	Sequence
C 153	9.2	48.4	19	2	CS197453	Sequence	C 226	9.2	47.4	19	2	CS197914	Sequence
C 154	9.2	48.4	19	2	CS197805	Sequence	C 227	9.2	47.4	19	2	CS199664	Sequence
C 155	9.2	48.4	19	2	CS197811	Sequence	C 228	9.2	47.4	19	2	CS199665	Sequence
C 156	9.2	48.4	19	2	CS199200	Sequence	C 229	9.2	47.4	19	2	CS199666	Sequence
C 157	9.2	48.4	19	2	CS199201	Sequence	C 230	9.2	47.4	19	2	DD174897	THERAPUT
C 158	9.2	48.4	19	2	CS199202	Sequence	C 231	9.2	47.4	19	2	DD174918	THERAPUT
C 159	9.2	48.4	19	2	CS199203	Sequence	C 232	9.2	47.4	19	2	DD174942	THERAPUT
C 160	9.2	48.4	19	2	CS199204	Sequence	C 233	9.2	47.4	19	2	DD174957	THERAPUT
C 161	9.2	48.4	19	2	CS199205	Sequence	C 234	9.2	47.4	19	2	DD174981	THERAPUT
C 162	9.2	48.4	19	2	CS199557	Sequence	C 235	9.2	47.4	19	2	DD175047	THERAPUT
C 163	9.2	48.4	19	2	CS199563	Sequence	C 236	9.2	47.4	19	2	DD175128	THERAPUT
C 164	9.2	48.4	19	2	CS203688	Sequence	C 237	9.2	47.4	19	2	DD175185	THERAPUT

C 238	9	47.4	19	2	DD197645	311	8.8	46.3	19	2	CQ961569	CQ961569 Sequence
C 239	9	47.4	19	2	DD197649	C 312	8.8	46.3	19	2	CQ961585	CQ961585 Sequence
C 240	9	47.4	19	2	DD197652	C 313	8.8	46.3	19	2	CQ961634	CQ961634 Sequence
241	9	47.4	19	2	DD197807	314	8.8	46.3	19	2	CQ961648	CQ961648 Sequence
242	9	47.4	19	2	DD198341	C 315	8.8	46.3	19	2	CQ962331	CQ962331 Sequence
243	9	47.4	19	2	DD198345	C 316	8.8	46.3	19	2	CQ962336	CQ962336 Sequence
C 244	9	47.4	19	2	DD198348	C 317	8.8	46.3	19	2	CQ965463	CQ965463 Sequence
C 245	9	47.4	19	2	DD198503	C 318	8.8	46.3	19	2	CQ965626	CQ965626 Sequence
C 246	9	47.4	19	2	DD202481	C 319	8.8	46.3	19	2	CQ966716	CQ966716 Sequence
C 247	9	47.4	19	2	DD202805	C 320	8.8	46.3	19	2	CQ966897	CQ966897 Sequence
C 248	9	47.4	19	2	DD204244	C 321	8.8	46.3	19	2	CQ96897	CQ96897 Sequence
C 249	9	47.4	19	2	DD204248	C 322	8.8	46.3	19	2	CS014347	CS014347 Sequence
C 250	9	47.4	19	2	DD204251	C 323	8.8	46.3	19	2	CS014627	CS014627 Sequence
C 251	9	47.4	19	2	DD204406	C 324	8.8	46.3	19	2	CS015041	CS015041 Sequence
252	9	47.4	19	2	DD204940	325	8.8	46.3	19	2	CS027812	CS027812 Sequence
253	9	47.4	19	2	DD204944	C 326	8.8	46.3	19	2	CS028172	CS028172 Sequence
254	9	47.4	19	2	DD204947	C 327	8.8	46.3	19	2	CS028279	CS028279 Sequence
C 255	9	47.4	19	2	DD205107	C 328	8.8	46.3	19	2	CS028639	CS028639 Sequence
C 256	9	47.4	19	2	DD205122	C 329	8.8	46.3	19	2	CS067596	CS067596 Sequence
257	9	47.4	19	2	E05126	C 330	8.8	46.3	19	2	CS083317	CS083317 Sequence
258	9	47.4	19	2	E42991	C 331	8.8	46.3	19	2	CS092930	CS092930 Sequence
259	9	47.4	19	2	I14060	C 332	8.8	46.3	19	2	CS093237	CS093237 Sequence
C 260	9	47.4	19	2	AR208209	C 333	8.8	46.3	19	2	CS094055	CS094055 Sequence
261	9	47.4	19	2	AR292691	C 334	8.8	46.3	19	2	CS094155	CS094155 Sequence
C 262	9	47.4	19	2	AR573111	C 335	8.8	46.3	19	2	CS096186	CS096186 Sequence
C 263	9	47.4	19	2	AR573618	336	8.8	46.3	19	2	CS096285	CS096285 Sequence
C 264	9	47.4	19	2	AX008562	C 337	8.8	46.3	19	2	CS101995	CS101995 Sequence
C 265	9	47.4	19	2	AX078717	C 338	8.8	46.3	19	2	CS102132	CS102132 Sequence
C 266	9	47.4	19	2	AX118522	C 339	8.8	46.3	19	2	CS105004	CS105004 Sequence
267	9	47.4	19	2	AX131221	C 340	8.8	46.3	19	2	CS122274	CS122274 Sequence
C 268	9	47.4	19	2	AX131728	C 341	8.8	46.3	19	2	CS128959	CS128959 Sequence
C 269	9	47.4	19	2	AX680263	C 342	8.8	46.3	19	2	CS132232	CS132232 Sequence
C 270	9	47.4	19	2	AX786428	C 343	8.8	46.3	19	2	CS141728	CS141728 Sequence
C 271	9	47.4	19	8	AB068706	C 344	8.8	46.3	19	2	CS145659	CS145659 Sequence
C 272	8.8	46.3	19	2	Al7177	C 345	8.8	46.3	19	2	CS162487	CS162487 Sequence
C 273	8.8	46.3	19	2	AR000431	C 346	8.8	46.3	19	2	CS165985	CS165985 Sequence
C 274	8.8	46.3	19	2	AR007328	C 347	8.8	46.3	19	2	CS187399	CS187399 Sequence
C 275	8.8	46.3	19	2	AR019627	348	8.8	46.3	19	2	CS189942	CS189942 Sequence
C 276	8.8	46.3	19	2	AR027560	349	8.8	46.3	19	2	CS190943	CS190943 Sequence
C 277	8.8	46.3	19	2	AR034262	350	8.8	46.3	19	2	CS193706	CS193706 Sequence
278	8.8	46.3	19	2	AR037229	C 351	8.8	46.3	19	2	CS193707	CS193707 Sequence
C 279	8.8	46.3	19	2	AR048698	C 352	8.8	46.3	19	2	CS204195	CS204195 Sequence
C 280	8.8	46.3	19	2	AR059343	C 353	8.8	46.3	19	2	CS250304	CS250304 Sequence
281	8.8	46.3	19	2	AR068747	C 354	8.8	46.3	19	2	CS251829	CS251829 Sequence
C 282	8.8	46.3	19	2	AR079435	C 355	8.8	46.3	19	2	CS254946	CS254946 Sequence
C 283	8.8	46.3	19	2	AX923158	C 356	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 284	8.8	46.3	19	2	AX925790	C 357	8.8	46.3	19	2	DD166272	DD166272 Methods o
C 285	8.8	46.3	19	2	AX930495	C 358	8.8	46.3	19	2	DD168615	DD168615 Novel Vec
C 286	8.8	46.3	19	2	AX934005	C 359	8.8	46.3	19	2	DD192070	DD192070 EMT INDUC
C 287	8.8	46.3	19	2	AX937243	C 360	8.8	46.3	19	2	DD200431	DD200431 RNA Inter
C 288	8.8	46.3	19	2	AX937264	C 361	8.8	46.3	19	2	DD200626	DD200626 RNA Inter
C 289	8.8	46.3	19	2	AX958893	C 362	8.8	46.3	19	2	DD200811	DD200811 RNA Inter
C 290	8.8	46.3	19	2	AX962272	C 363	8.8	46.3	19	2	DD201578	DD201578 RNA Inter
C 291	8.8	46.3	19	2	BD023617	364	8.8	46.3	19	2	DD201828	DD201828 RNA Inter
C 292	8.8	46.3	19	2	BD196880	C 365	8.8	46.3	19	2	DD202005	DD202005 RNA Inter
C 293	8.8	46.3	19	2	CQ753338	C 366	8.8	46.3	19	2	DD202255	DD202255 RNA Inter
C 294	8.8	46.3	19	2	CQ761102	C 367	8.8	46.3	19	2	DD203139	DD203139 RNA Inter
C 295	8.8	46.3	19	2	CQ768128	C 368	8.8	46.3	19	2	DD203386	DD203386 RNA Inter
C 296	8.8	46.3	19	2	CQ785954	C 369	8.8	46.3	19	2	DD206040	DD206040 RNA Inter
C 297	8.8	46.3	19	2	CQ787631	C 370	8.8	46.3	19	2	DD206454	DD206454 RNA Inter
C 298	8.8	46.3	19	2	CQ788889	C 371	8.8	46.3	19	2	E37395	E37395 Synthetic n
299	8.8	46.3	19	2	CQ793272	C 372	8.8	46.3	19	2	AR216662	AR216662 Sequence
C 300	8.8	46.3	19	2	CQ812671	C 373	8.8	46.3	19	2	AR271393	AR271393 Sequence
C 301	8.8	46.3	19	2	CQ813497	C 374	8.8	46.3	19	2	AR293417	AR293417 Sequence
C 302	8.8	46.3	19	2	CQ819460	C 375	8.8	46.3	19	2	AR295891	AR295891 Sequence
C 303	8.8	46.3	19	2	CQ821862	C 376	8.8	46.3	19	2	177073	177073 Sequence 34
C 304	8.8	46.3	19	2	CQ856049	377	8.8	46.3	19	2	189288	189288 Sequence 49
C 305	8.8	46.3	19	2	CQ955918	C 378	8.8	46.3	19	2	AR571808	AR571808 Sequence
C 306	8.8	46.3	19	2	CQ959934	C 379	8.8	46.3	19	2	AR572263	AR572263 Sequence
C 307	8.8	46.3	19	2	CQ959983	C 380	8.8	46.3	19	2	AR572264	AR572264 Sequence
C 308	8.8	46.3	19	2	CQ959997	C 381	8.8	46.3	19	2	AR654660	AR654660 Sequence
309	8.8	46.3	19	2	CQ960680	C 382	8.8	46.3	19	2	AX021827	AX021827 Sequence
C 310	8.8	46.3	19	2	CQ960685	C 383	8.8	46.3	19	2	AX129918	AX129918 Sequence
											AX130373	AX130373 Sequence

C 384	8.8	46.3	19	2	AX130374	AX130374 Sequence	C 457	8.6	45.3	19	2	DD204220	DD204220 RNA Inter
C 385	8.8	46.3	19	2	AX473974	AX473974 Sequence	C 458	8.6	45.3	19	2	DD204229	DD204229 RNA Inter
C 386	8.8	46.3	19	2	AX473978	AX473978 Sequence	C 459	8.6	45.3	19	2	DD204410	DD204410 RNA Inter
C 387	8.8	46.3	19	2	AX571906	AX571906 Sequence	C 460	8.6	45.3	19	2	DD204411	DD204411 RNA Inter
C 388	8.8	46.3	19	2	AX805585	AX805585 Sequence	C 461	8.6	45.3	19	2	DD204916	DD204916 RNA Inter
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C 396	8.6	45.3	19	2	AR145159	AR145159 Sequence	C 469	8.6	45.3	19	2	AR235571	AR235571 Sequence
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546	8.4	44.2	19	2	CS090615	Sequence	619	8.4	44.2	19	2	E32522	Scavenger r
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					124222	Dog (Clone

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	ORIGIN	Query Match	Best Local Similarity	Matches	QY	Db	RESULT 2	LOCUS	DEFINITION	AX411929	AY411929	Sequence 29 from Patent WO0226968.	19 bp	DNA	linear	PAT 14-JUN-2002
AR451384	AR451384	Sequence 29 from patent US 6673917.	AR451384	AR451384.1 GI:42682409	Unknown.	Unclassified.	1 (bases 1 to 19)	Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.	Antisense iAP nucleic acids and uses thereof	Patent: US 6673917-A 29 06-JAN-2004; University of Ottawa; Ottawa; CAX;	location/Qualifiers 1..19 /organism="unknown" /mol_type="genomic DNA"	100.0%; Score 19; DB 2; Length 19;	100.0%; Pred. No. 85;	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 CGCAGCGTATCTCCTTCAC 19	1 CGCAGCGTATCTCCTTCAC 19	CGCAGCGTATCTCCTTCAC 19	AX411929	AY411929	Sequence 29 from Patent WO0226968.	19 bp	DNA	linear	PAT 14-JUN-2002		

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VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.		
TITLE	Antisense iap nucleic acids and uses thereof		
JOURNAL	Patent: WO 026968-A 29 04-APR-2002;		
	University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)		
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Best Local Similarity	100.0%;	Pred. No. 85;	
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RESULT 3			
LOCUS	CS027764/c	19 bp	RNA
DEFINITION	Sequence 17 from Patent WO2005014811.	linear	PAT 03-MAR-2005
ACCESSION	CS027764		
VERSION	CS027764.1		
KEYWORDS	GI:60497314		
SOURCE			
ORGANISM	synthetic construct		
	synthetic construct		
	other sequences; artificial sequences.		
REFERENCE			
AUTHORS	1 Meswigen, J. and Chowrira, B.M.		
TITLE	RNA interference mediated inhibition of XIAP gene expression using		
JOURNAL	short interfering Nucleic Acid (siNA)		
	Patent: WO 2005014811-A 17 17-FEB-2005;		
	SiRNA Therapeutics, Inc. (US)		
FEATURES			
source	1..19		
	/organism="synthetic construct"		
	/mol_type="unassigned RNA"		
	/db_xref="taxon:32630"		
	/note="Description of Artificial Sequence: Target		
	Sequence/siNA sense region"		
ORIGIN			
Query Match	78.9%;	Score 15;	DB 2; Length 19;
Best Local Similarity	100.0%;	Pred. No. 1.3e+04;	
Matches	15; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
Qy	5 CGGTATCTCCTTCAC 19		
	19 CGGTATCTCCTTCAC 5		
RESULT 4			
LOCUS	CS028231	19 bp	RNA
DEFINITION	Sequence 484 from Patent WO2005014811.	linear	PAT 03-MAR-2005
ACCESSION	CS028231		
VERSION	CS028231.1		
KEYWORDS	GI:60497781		
SOURCE			
ORGANISM	synthetic construct		
	synthetic construct		
	other sequences; artificial sequences.		
REFERENCE			

AUTHORS Mcswiggen,J. and Chowrira,B.M.
TITLE RNA interference mediated inhibition of XIAP gene expression using
short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005014811-A 484 17-FEB-2005;
Sirta Therapeutics, Inc. (US)

FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: siNA antisense
region"

ORIGIN

Query Match 78.9%; Score 15; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGTATCTCTCTTCAC 19
| | | | | | | | | | | | | | | | | | | | |
Db 1 CGGTATCTCTCTTCAC 15

RESULT 5
AX923594 19 bp DNA linear PAT 18-DEC-2003
LOCUS AX923594
DEFINITION Sequence 29 from Patent WO03080638.
ACCESSION AX923594
VERSION AX923594.1 GI:40216610
KEYWORDS
ORGANISM
SOURCE
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Lacasse,E., Mcmanus,D. and Durkin,J.P.
TITLE Antisense iap nucleobase oligomers and uses thereof
JOURNAL Patent: WO 03080638-A 29 02-OCT-2003;
Aegera Therapeutics Inc. (CA)

FEATURES
source
1. .19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="based on Homo sapiens. Each nucleobase may be part
of a ribonucleotide, deoxyribonucleotide, or nucleotide
analog
n = T or U"

ORIGIN

Query Match 73.7%; Score 14; DB 2; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.8e+04;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTCAC 19
| | | | | | | | | | | | | | | | | | | | |
Db 1 CGCAGCGNANCCNNCAC 19

RESULT 6
AX923672 19 bp DNA linear PAT 18-DEC-2003
LOCUS AX923672
DEFINITION Sequence 107 from Patent WO03080638.
ACCESSION AX923672
VERSION AX923672.1 GI:40216688
KEYWORDS
SOURCE
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Lacasse,E., Mcmanus,D. and Durkin,J.P.
TITLE Antisense iap nucleobase oligomers and uses thereof
JOURNAL Patent: WO 03080638-A 107 02-OCT-2003;
Aegera Therapeutics Inc. (CA)

FEATURES
source
Location/Qualifiers
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="based on Homo sapiens. Each nucleobase may be part
of a ribonucleotide, deoxyribonucleotide, or nucleotide
analog
n = T or U"

ORIGIN

Query Match 73.7%; Score 14; DB 2; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.8e+04;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTCAC 19
| | | | | | | | | | | | | | | | | | | | |
Db 1 CGCAGCGNANCCNNCAC 19

RESULT 7
BD080793 19 bp DNA linear PAT 27-AUG-2002
LOCUS BD080793
DEFINITION Human estrogen receptor beta.
ACCESSION BD080793
VERSION BD080793.1 GI:22626396
KEYWORDS UP 2001510690-A/16.
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 19)

REFERENCE
AUTHORS Denton,R. and Barton,R.
TITLE Human estrogen receptor beta
JOURNAL Patent: JP 2001510690-A 16 07-AUG-2001;
YALB UNIVERSITY
OS Artificial Sequence
PN JP 2001510690-A/16
PD 07-AUG-2001 JP 2000504163
PF 28-JUL-1998 JP 2000504163
PR 28-JUL-1997 US 60/053869,30-JUL-1997 US 60/054210 PI
REX DENTON,ROLAND BARON
PC

C12N15/09,A61K31/711,A61K38/00,A61K39/395,A61K39/395,A61K45/00, PC
A61K48/00,
PC A61P35/00,A61P43/00,C07K14/705,C07K16/28,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,G01N33/15,G01N33/50, PC
G01N33/53,
PC G01N33/566,C12N15/00,A61K37/02,C12N5/00
CC Description of Artificial Sequence: Cloning/PCR primer, primer

FEATURES
source
1. .19
Location/Qualifiers
/organism="Artificial Sequence".
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 62.1%; Score 11.8; DB 2; Length 19;
Best Local Similarity 86.7%; Pred. No. 7.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGTATCTCTCTTCAC 19
| | | | | | | | | | | | | | | | | | | | |
Db 2 CAGTACTCTCTTCAC 16

RESULT 8
BD080808

LOCUS	B08080608	19 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Novel estrogen receptor beta and iso-type proteins thereof.				
ACCESSION	B08080608				
VERSION	B08080808.1	GI:22626411			
KEYWORDS	JP 2001510691-A/11.				
SOURCE	JP 2001510691-A/11.				
ORGANISM	synthetic construct synthetic construct other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 19) Baron,R., Denton,R., Chambon,P., Dupont,S. and Garnier,J.M. Novel estrogen receptor beta and iso-type proteins thereof Patent: JP 2001510691-A 11 07-AUG-2001;				
AUTHORS	YALE UNIVERSITY				
TITLE					
JOURNAL	OS Artificial Sequence PN JP 2001510691-A/11				
COMMENT	PD 07-AUG-2001 PF 28-JUL-1998 JP 2000504164 PR 28-JUL-1997 US 60/053869,30-JUL-1997 US 60/054210 PR 28-JUL-1997 US 60/053869,30-JUL-1997 US 60/054210 PI ROLAND BARON,REX DENTON,PIERRE CHAMBON,SONIA DUPONT,JEAN MARIE PI GARNIER PC C12N15/09,A61K31/7088,A61K38/00,A61K39/395,A61K39/395 PC A61K39/395,A61K51/00, PC A61K48/00,A61P13/08,A61P19/10,A61P35/00,C07K14/47,C07K14/705, PC C07K16/28, PC C07K16/46,C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/566, PC C12M15/00, PC A61K37/02,A61K43/00,C12N5/00 CC Description of Artificial Sequence: Cloning/PCR primer, primer				
FEATURES	source				
ORIGIN	CC CC 7 FH FH Location/Qualifiers FT source 1..19 FT /organism='Artificial Sequence'. location/Qualifiers 1..19 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"				
Query Match	62.1%;	Score 11.8;	DB 2;	Length 19;	
Best Local Similarity	86.7%;	Pred. No. 7.8e+05;			
Matches 13;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
Oy	5 CGGTATCGCTTCAC 19				
Db	2 CAGTAGCTCCTTCCAC 16				
RESULT 9					
CS251594/c	CS251594	19 bp	DNA	linear	PAT 18-JAN-2006
LOCUS	Sequence 161 from Patent WO2005124342.				
DEFINITION	CS251594				
ACCESSION	CS251594				
VERSION	CS251594.1	GI:85362134			
KEYWORDS	.				
SOURCE	synthetic construct synthetic construct other sequences; artificial sequences.				
ORGANISM	1 Vandeghinste,N. Methods and means for treatment of osteoarthritis Patent: WO 2005124342-A 161 29-DEC-2005; Galapagos N.V. (BE)				
REFERENCE	Location/Qualifiers 1..19 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Synthetic oligonucleotide"				
AUTHORS					
TITLE					
JOURNAL					
FEATURES	source				
ORIGIN					

Query Match	52.1%;	Score 11.8;	DB 2;	Length 19;
Best Local Similarity	86.7%;	Pred. No. 7.8e+05;		
Matches	13;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
Oy	5	CGGTATCTCCTTCAC	19	
Db	17	CAGTATCTCCTTCAC	3	
RESULT 10				
LOCUS	CS094047	19 bp	RNA	
DEFINITION	Sequence 39 from Patent WO2005045041.		linear	PAT 03-JUN-2005
ACCESSION	CS094047			
VERSION	CS094047.1	GI:66951561		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	1	McSwiggen,J. and Polisky,B.		
TITLE		RNA interference mediated inhibition of cholesterol ester transfer protein (cebp) gene expression using short interfering nucleic acid (siRNA)		
JOURNAL		Patent: WO 2005045041-A 39 19-MAY-2005;		
FEATURES				
SOURCE		SiRNA Therapeutics, Inc. (US)		
		Location/Qualifiers		
	1..19	/organism="synthetic construct"		
		/mol_type="unassigned RNA"		
		/db_xref="taxon:32630"		
		/note="Description of Artificial Sequence: Target/siNA sense"		
ORIGIN				
Query Match	57.9%;	Score 11;	DB 2;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 2.1e+06;		
Matches	11;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Oy	9	ATCTCCTTCAC	19	
Db	6	ATCTCCTTCAC	16	
RESULT 11				
LOCUS	CS094147	19 bp	RNA	
DEFINITION	Sequence 139 from Patent WO2005045041.		linear	PAT 03-JUN-2005
ACCESSION	CS094147			
VERSION	CS094147.1	GI:66951661		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	1	McSwiggen,J. and Polisky,B.		
TITLE		RNA interference mediated inhibition of cholesterol ester transfer protein (cebp) gene expression using short interfering nucleic acid (siRNA)		
JOURNAL		Patent: WO 2005045041-A 139 19-MAY-2005;		
FEATURES				
SOURCE		SiRNA Therapeutics, Inc. (US)		
		Location/Qualifiers		
	1..19	/organism="synthetic construct"		
		/mol_type="unassigned RNA"		
		/db_xref="taxon:32630"		
		/note="Description of Artificial Sequence: Target/siNA sense"		
ORIGIN				
Query Match	57.9%;	Score 11;	DB 2;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 2.1e+06;		

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATCTCTTCAC 19
|||||
14 ATCTCTTCAC 4

Db

RESULT 12
AR295824
LOCUS AR295824 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7559 from patent US 6537751.
ACCESSION AR295824
VERSION AR295824.1 GI:31683108
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7559 25-MAR-2003;
Genet S.A.;;
FRX;

FEATURES
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 57.9%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2,1e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GATCTCTTC 17
|||||
1 GATCTCTTC 11

Db

RESULT 13
AR573706/c
LOCUS AR573706 19 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 3034 from patent US 6770633.
ACCESSION AR573706
VERSION AR573706.1 GI:56574598
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: US 6770633-A 3034 03-AUG-2004;
Immusol, Inc.; San Diego, CA
location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 56.8%; Score 10.8; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 2,8e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTCA 18
|||||
17 CGGTCTACTCA 4

Db

RESULT 14
AR573800
LOCUS AR573800 19 bp DNA linear PAT 14-DEC-2004

DEFINITION Sequence 3128 from patent US 6770633.
ACCESSION AR573800
VERSION AR573800.1 GI:56574692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: US 6770633-A 3128 03-AUG-2004;
Immusol, Inc.; San Diego, CA
location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 56.8%; Score 10.8; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 2,8e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTCA 18
|||||
6 CAGTTCTCCTCA 19

Db

RESULT 15
AR573801
LOCUS AR573801 19 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 3129 from patent US 6770633.
ACCESSION AR573801
VERSION AR573801.1 GI:56574693
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: US 6770633-A 3129 03-AUG-2004;
Immusol, Inc.; San Diego, CA
location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 56.8%; Score 10.8; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 2,8e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTCA 18
|||||
5 CAGTTCTCCTCA 18

Db

RESULT 16
AR573802
LOCUS AR573802 19 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 3130 from patent US 6770633.
ACCESSION AR573802
VERSION AR573802.1 GI:56574694
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases

JOURNAL Patent: US 6770633-A 3130 03-AUG-2004;

source	FEATURES
1. .19	Immunosol, Inc.; San Diego, CA Location/Qualifiers

ORIGIN

Query Match	56.8%	Score 10.8;	DB 2;	length 19;
Best Local Similarity	85.7%	Pred. No. 2.8e+06;		
Matches 12; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	5	CGGATCTCCTTCA	18
Db	4	CAGTTCTCCTTCA	17

RESULT 17	LOCUS	AR573803	19 bp	DNA	linear	PAT 14-DEC-2004
DEFINITION	AR573803	Sequence 3131 from patent US 6770633.				

Unclassified

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 19)	Robbins, J.M. and Tritz, R.	Ribozyme therapy for the treatment of proliferative skin and eye

JOURNAL
Patent: US 6770633-A 3131 03-AUG-2004;
Immusol, Inc.; San Diego, CA

FEATURES	Location/Qualifiers
source	1. .19

ORIGIN

Query Match	56.8%	Score 10.8;	DB 2;	Length 19;
Best Local Similarity	85.7%	Pred. No. 2.8e+06;		
Matches 12;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	5	CGGTATCTCCTTCA	18
Db	2	CAGTTTCTCCCTTCA	15

RESULT 18	
AX131816/c	
LOCUS	AX131816
DEFINITION	Sequence 3034 from Patent WO0130362.
	19 bp DNA
	linear
	PAT 15-MAY-2001

SOURCE ORGANISM	
Homo sapiens (human)	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	

REFERENCE	AUTHORS	TITLE
1	Robbins, J.M. and Trletz, R.	Ribozyme therapy for the treatment of proliferative skin and eye diseases

JOURNAL Patent: WO 0130362-A 3034 03-MAY-2001;
IMMUSOL, INC. (US)

FEATURES	Location/Qualifiers
source	1. .19

ORIGIN

Query Match	56.8%	Score 10.8;	DB 2;	Length 19;
Best Local Similarity	85.7%;	Pred. No. 2.8e+06;		
Matches 12; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	5	CGGATCTCCTTCA	18
Db	17	CGGTGCTACTTCA	4

RESULT 19	AX131910	19 bp	DNA	linear	PAT 15-MAY-2001
LOCUS	AX131910				
DEFINITION	Sequence 3128 from Patent WO0130362.				
ACCESSION	AX131910				
VERSION	AX131910.1	GI:14138215			

SOURCE ORGANISM	
Homo sapiens (human)	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	

Robbins, J.M. and Tritz, R.

JOURNAL
Diseases
Patent: WO 0130362-A 3128 03-MAY-2001;
IMMUSOL, INC. (US)

FEATURES	Location/Qualifiers
source	1. .19

ORIGIN

Query Match	56.8%	Score 10.8;	DB 2;	Length 19;
Best Local Similarity	85.7%;	Pred. No. 2.8e+06;		
Matches 12;	Conservative	2;	Indels 0;	Gaps 0;

QY	5	CGGTATCTCCTTCA	18
Db	6	CAGTTTCTCCTTCA	19

RESULT 20			
AX131911			
LOCUS			
DEFINITION			
AX131911	19 bp	DNA	linear
Sequence 3129	from Patent	WO0130362.	PAT 15-MAY-2001

SOURCE	ORGANISM
Homo sapiens (human)	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS	TITLE
Robbins, J.M. and Tiltz, R.	Ribozyme therapy for the treatment of proliferative skin and eye diseases

IMMUSOL, INC. (US)
Location/Qualifiers

```
source      l. .19
            /organism="Homo sapiens"
```

ORIGIN

Query Match	56.8%;	Score 10.8;	DB 2;	Length 19;
Best Local Similarity	85.7%;	Pred. No. 2.8e+06;		

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGTATCTCTTCA 18
Db 5 CAGTTCTCTTCA 18

RESULT 21
AX131912
LOCUS
DEFINITION Sequence 3130 from Patent WO0130362.
ACCESSION AX131912
VERSION AX131912.1 GI:14138217
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Robbins J.M. and Tritz R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 3130 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
SOURCE location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin A1 ribozyme binding site"

ORIGIN
Query Match 56.8%; Score 10.8; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 2.8e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGTATCTCTTCA 18
Db 4 CAGTTCTCTTCA 17

RESULT 22
AX131913
LOCUS
DEFINITION Sequence 3131 from Patent WO0130362.
ACCESSION AX131913
VERSION AX131913.1 GI:14138218
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Robbins J.M. and Tritz R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 3131 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
SOURCE location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin A1 ribozyme binding site"

ORIGIN
Query Match 56.8%; Score 10.8; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 2.8e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGTATCTCTTCA 18

Db 2 CAGTTCTCTTCA 15

RESULT 23
CO824220
LOCUS
DEFINITION Sequence 73 from Patent EP1428893.
ACCESSION CO824220
VERSION CO824220.1 GI:49021193
KEYWORDS
SOURCE
ORGANISM
SOURCE
REFERENCE
AUTHORS Sprecher, E. and Bergman, R.
TITLE Methods of and compositions for modulating hair growth via p-cadherin modulators
JOURNAL Patent: EP 1428893-A 73 16-JUN-2004;
Sprecher, Eli (IL); Bergman, Reuven (IL)
FEATURES
SOURCE location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN
Query Match 55.8%; Score 10.6; DB 2; Length 19;
Best Local Similarity 76.5%; Pred. No. 3.6e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CACGTATCTCTTCA 19
Db 3 CGCGGCGCTGCTTCA 19

RESULT 24
CS171759
LOCUS
DEFINITION Sequence 5004 from Patent EP1580263.
ACCESSION CS171759
VERSION CS171759.1 GI:77156429
KEYWORDS
SOURCE
ORGANISM
SOURCE
REFERENCE
AUTHORS Ieagol, T.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1580263-A 5004 28-SEP-2005;
Research Association for Biotech nology (JP)
FEATURES
SOURCE location/Qualifiers
1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of Artificial Sequence: an artificially synthesized primer se q uence"

ORIGIN
Query Match 55.8%; Score 10.6; DB 2; Length 19;
Best Local Similarity 76.5%; Pred. No. 3.6e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CACGTATCTCTTCA 19
Db 1 CACTGATTTCTTCA 17

RESULT 25
E54494/c
LOCUS
E54494 19 bp DNA linear PAT 27-AUG-2002

DEFINITION Heat-resistant lysine biosynthesis enzyme gene of thermophilic
 Corynebacterium.
 ACCESSION E54494
 VERSION E54494.1 GI:22553551
 KEYWORDS JP 2001120270-A/18.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Itaya,M., Kimura,E., Kawara,Y. and Sugimoto,S.
 TITLE Heat-resistant lysine biosynthesis enzyme gene of thermophilic
 JOURNAL coryneform bacterium
 COMMENT Patent: JP 2001120270-A 18 08-MAY-2001;
 AJINOMOTO CO INC
 OS Artificial Sequence
 PN JP 2001120270-A/18
 PD 08-MAY-2001
 PP 01-NOV-1999 JP 1999311148
 P1 MINORU ITAYA,EICHIRO KIMURA,YOSHIO KAWARA,SHINICHI SUGIMOTO PC
 C12N15/09/(C12N15/09,C12R1:15),C12N15/00,C12R1:15) CC
 Description of Artificial Sequence: primer for LA cloning of CC
 FEATURES
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 55.8%; Score 10.6; DB 2; Length 19;
 Best Local Similarity 76.5%; Pred. No. 3.6e+06;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 GCACGATCTCTCTTCA 18
 DB 17 GTACGGCATCGCTTACA 1

RESULT 26
 AR297589/c 19 bp DNA linear PAT 12-JUN-2003
 LOCUS AR297589
 DEFINITION Sequence 9324 from patent US 6537751.
 ACCESSION AR297589
 VERSION AR297589.1 GI:31684873
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
 TITLE Biallelic markers for use in constructing a high density
 JOURNAL disequilibrium map of the human genome
 Patent: US 6537751-A 9324 25-MAR-2003;
 Genet S.A.;?
 FRX;
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 Location/Qualifiers
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 /mol_type="genomic DNA"

Query Match 55.8%; Score 10.6; DB 2; Length 19;
 Best Local Similarity 76.5%; Pred. No. 3.6e+06;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CACGATCTCTCTTCA 19
 DB 19 CACAGTCTCTTTTCAC 3

RESULT 27
 AX117403

LOCUS AX117403 19 bp DNA linear PAT 11-MAY-2001
 DEFINITION Sequence 2526 from Patent WO0129262.
 ACCESSION AX117403
 VERSION AX117403.1 GI:14034354
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Picoult-Newburg,L. and Pohl,M.
 TITLE Genotyping reagents, kits and methods of use thereof
 JOURNAL Patent: WO 0129262-A 2526 26-APR-2001;
 Orchid Biosciences, Inc. (US)
 FEATURES
 source 1..19
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer"

Query Match 55.8%; Score 10.6; DB 2; Length 19;
 Best Local Similarity 76.5%; Pred. No. 3.6e+06;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 CACGATCTCTCTTCA 19
 DB 1 CACGGTTTCACCTTCCC 17

RESULT 28
 AX751584 19 bp DNA linear PAT 20-JUN-2003
 LOCUS AX751584
 DEFINITION Sequence 5 from Patent WO03034072.
 ACCESSION AX751584
 VERSION AX751584.1 GI:32133863
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Wilson,D.I., Hearn,T. and Walker,M.
 TITLE Diagnosis and therapy of conditions involving ALMS1
 JOURNAL Patent: WO 03034072-A 5 24-APR-2003;
 UNIVERSITY OF SOUTHAMPTON (GB)
 FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:32630"
 /note="Primer"

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 Best Local Similarity 76.5%; Pred. No. 3.6e+06;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GCACGATCTCTCTTCA 18
 DB 1 GCGCGTTTCTCTCGTCA 17

RESULT 29
 AX837880 19 bp DNA linear PAT 15-DEC-2003
 LOCUS AX837880
 DEFINITION Sequence 5004 from Patent EP1347046.
 ACCESSION AX837880
 VERSION AX837880.1 GI:39921572
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1 unclassified sequences.

AUTHORS Isegaki, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.

TITLE Full-length cDNA sequences

JOURNAL Patent: EP 1347046-A 5004 24-SEP-2003; Research Association for Biotechnology (JP)

FEATURES
source
1. 19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of Artificial Sequence: an artificially synthesized primer sequence"

ORIGIN

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Best Local Similarity 76.5%; Pred. No. 3.6e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 CACGATCTCCTTCAC 19
||| ||| ||| ||| |||
1 CACTGATTTTCTTCAC 17

RESULT 30
LOCUS CS246174 19 bp DNA linear PAT 09-JAN-2006
DEFINITION Sequence 113 from Patent WO2005119262.
ACCESSION CS246174
VERSION CS246174.1 GI:84660126
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE
AUTHORS Merckliere, P. G.
TITLE Methods, compositions and compound assays for inhibiting amyloid-beta protein production
JOURNAL Patent: WO 2005119262-A 113 15-DEC-2005; Galapagos Genomics N.V. (BE)

FEATURES
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1. 19
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

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Query Match 54.7%; Score 10.4; DB 2; Length 19;
Best Local Similarity 91.7%; Pred. No. 4.6e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 GGTATCTCCTTC 17
||| ||| ||| ||| |||
1 GGCACTCTCCTTC 12

Db

RESULT 31
LOCUS AR293205 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4940 from patent US 6537751.
ACCESSION AR293205
VERSION AR293205.1 GI:31680489
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 4940 25-MAR-2003;

Genet S.A.;

FRX;

FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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Best Local Similarity 91.7%; Pred. No. 4.6e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GATCTCCTTCA 18
||| ||| ||| ||| |||
2 GTATCTACTTCA 13

Db

RESULT 32
LOCUS AR294484 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6219 from patent US 6537751.
ACCESSION AR294484
VERSION AR294484.1 GI:31681768
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 6219 25-MAR-2003; Genet S.A.;

FEATURES
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ORIGIN

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Best Local Similarity 91.7%; Pred. No. 4.6e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 TATCTCCTTCAC 19
||| ||| ||| ||| |||
4 TATCTACTTCAC 15

Db

RESULT 33
LOCUS AR533333 19 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 18 from patent US 6730500.
ACCESSION AR533333
VERSION AR533333.1 GI:53922961
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS Lok, S.
TITLE Methods for generating a continuous nucleotide sequence from noncontiguous nucleotide sequences
JOURNAL Patent: US 6730500-A 18 04-MAY-2004; ZymoGenetics, Inc.; Seattle, WA

FEATURES
source
1. 19
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ORIGIN

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Best Local Similarity 91.7%; Pred. No. 4.6e+06;

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QY 4 ACGGATCTCCT 15
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Db 18 AAGGATCTCCT 7

RESULT 34
AR573804
LOCUS AR573804 19 bp DNA
DEFINITION Sequence 3132 from patent US 6770633.
ACCESSION AR573804
VERSION AR573804.1 GI:56574696
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 19)
  Robbins,J.M. and Tritz,R.
  Ribozyme therapy for the treatment of proliferative skin and eye
  diseases
  Patent: US 6770633-A 3132 03-AUG-2004;
  Immusol, Inc.; San Diego, CA
  Location/Qualifiers
    1..19
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    /mol_type="genomic DNA"

ORIGIN
Query Match 54.7%; Score 10.4; DB 2; Length 19;
Best Local Similarity 91.7%; Pred. No. 4.6e+06;
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QY 7 GTATCTCCTCA 18
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Db 1 GTTCTCCTTCA 12

RESULT 35
AX131914
LOCUS AX131914 19 bp DNA
DEFINITION Sequence 3132 from Patent WO0130362.
ACCESSION AX131914
VERSION AX131914.1 GI:14138219
KEYWORDS
SOURCE
ORGANISM
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
  1
  Robbins,J.M. and Tritz,R.
  Ribozyme therapy for the treatment of proliferative skin and eye
  diseases
  Patent: WO 0130362-A 3132 03-MAY-2001;
  IMMUSOL, INC. (US)
  Location/Qualifiers
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    /db_xref="taxon:9606"
    /note="Cyclin A1 ribozyme binding site"

ORIGIN
Query Match 54.7%; Score 10.4; DB 2; Length 19;
Best Local Similarity 91.7%; Pred. No. 4.6e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTATCTCCTCA 18
    |||||
Db 1 GTTCTCCTTCA 12

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RESULT 36
BD244859/c
LOCUS BD244859 19 bp DNA
DEFINITION Oligonucleotide primer capable of making the non-specific double
  strand formation unstable.
ACCESSION BD244859
VERSION BD244859.1 GI:33054629
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 19)
  Pelletier,J. and Das,M.
  Oligonucleotide primer capable of making the non-specific double
  strand formation unstable
  Patent: JP 2002532063-A 4 02-OCT-2002;
  MCGILL UNIVERSITY
  OS Artificial Sequence
  PN JP 2002532063-A/4
  PD 02-OCT-2002
  PR 06-OCT-1999 JP 2000574722
  PR 07-OCT-1998 CA 2246623
  PI JERRY PELLETIER, MANJULA DAS
  CC C12N15/09,C12Q1/68,C12N15/00
  CC Description of Artificial Sequence: synthetic oligonucleotide
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  FT source
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      /mol_type="genomic DNA"
      /db_xref="taxon:32630"

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Best Local Similarity 80.0%; Pred. No. 5.9e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CACGATCTCCTTC 17
    |||||
Db 15 CACAGATTTCTTC 1

RESULT 37
CS128821/c
LOCUS CS128821 19 bp DNA
DEFINITION Sequence 2 from Patent WO2005063983.
ACCESSION CS128821
VERSION CS128821.1 GI:71790688
KEYWORDS
SOURCE
ORGANISM
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
  1
  van Rompaey,L.J.
  Patent: WO 2005063983-A 2 14-JUL-2005;
  Galapagos Genomics N.V. (BB)
  Location/Qualifiers
    1..19
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

ORIGIN
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Best Local Similarity 80.0%; Pred. No. 5.9e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 CGGATCTCCTTCA 19
    |||||

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Db 16 CAGCAGCTCTTCAC 2

RESULT 38
LOCUS CS132095/c 19 bp DNA linear PAT 02-AUG-2005
DEFINITION Sequence 4 from Patent WO2005063976.
ACCESSION CS132095
VERSION CS132095.1 GI:71795131
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1
TITLE Van Rompaey, L.J.
JOURNAL Methods for inducing differentiation of undifferentiated mammalian cells into osteoblasts
PATENT: WO 2005063976-A 4 14-JUL-2005;
Galapagos Genomics N.V. (BE)
FEATURES
source location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN
Query Match 53.7%; Score 10.2; DB 2; Length 19;
Best Local Similarity 80.0%; Pred. No. 5.9e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGGTATCTCTTCAC 19
Db 16 CAGCAGCTCTTCAC 2

RESULT 39
LOCUS CS197806 19 bp RNA linear PAT 08-DEC-2005
DEFINITION Sequence 1329 from Patent WO2005105995.
ACCESSION CS197806
VERSION CS197806.1 GI:83413293
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1
JOURNAL Mcswigen, J.
PATENT: WO 2005105995-A 1329 10-NOV-2005;
Sirna Therapeutics, Inc. (US)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Synthetic"

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Best Local Similarity 80.0%; Pred. No. 5.9e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTT 16
Db 5 GCACGGTATCTCCTT 19

RESULT 40
LOCUS CS197807 19 bp RNA linear PAT 08-DEC-2005
DEFINITION Sequence 1330 from Patent WO2005105995.
ACCESSION CS197807
VERSION CS197807.1 GI:83413294

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
FEATURES
source
ORIGIN
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Best Local Similarity 80.0%; Pred. No. 5.9e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTT 16
Db 4 GCACGGTATCTCCTT 18

Search completed: August 10, 2006, 09:31:31
Job time : 1006.67 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: August 10, 2006, 07:08:17 ; Search time 981 Seconds
(without alignments)
1238.533 Million cell updates/sec

Title: US-10-636-065-29

Perfect score: 19

Sequence: 1 cgcacggatccctccac 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2541152

Minimum DB seq length: 0

Maximum DB seq length: 70

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl:*
1: gb env:*
2: gb pat:*
3: gb ph:*
4: gb pl:*
5: gb pr:*
6: gb ro:*
7: gb stb:*
8: gb sy:*
9: gb un:*
10: gb vi:*
11: gb ov:*
12: gb htg:*
13: gb in:*
14: gb om:*
15: gb ba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	19	100.0	19	2	AR451384 Sequence
2	19	100.0	19	2	AX411929 Sequence
3	18	94.7	23	2	AR103283 Sequence
4	15.4	81.1	54	2	AR559550 Sequence
5	15	78.9	19	2	CS027764 Sequence
6	15	78.9	19	2	CS028231 Sequence
7	14	73.7	19	2	AX923594 Sequence
8	14	73.7	19	2	AX923672 Sequence
9	13.8	72.6	59	2	AR356378 Sequence
10	13.8	72.6	59	2	AR356378 Sequence
11	13.4	70.5	37	2	AR537934 Sequence
12	13.4	70.5	37	2	AR537934 Sequence
13	13.4	70.5	40	5	S80712 gamma delta
14	13.4	69.5	60	2	AR311923 Sequence
15	13.2	69.5	29	2	AR721266 Sequence
16	13.2	69.5	42	2	AR525902 Sequence
17	13.2	69.5	56	2	AR526230 Sequence
18	13.2	69.5	65	2	CO531296 Sequence

C 19	12.8	67.4	22	2	BD074491	BD074491 Genetic r
C 20	12.8	67.4	22	2	AR569453	AR569453 Sequence
C 21	12.8	67.4	22	2	AX005818	AX005818 Sequence
C 22	12.8	67.4	23	2	BD074493	BD074493 Genetic r
C 23	12.8	67.4	23	2	AR569455	AR569455 Sequence
C 24	12.8	67.4	23	2	AX005820	AX005820 Sequence
C 25	12.8	67.4	52	2	AR580727	AR580727 Sequence
C 26	12.6	66.3	30	2	BD000514	BD000514 Method fo
C 27	12.6	66.3	30	2	DD159756	DD159756 Method fo
C 28	12.6	66.3	34	2	A06937	A06937 F.domebctcu
C 29	12.6	66.3	35	2	CQ970331	CQ970331 Sequence
C 30	12.6	66.3	35	2	CQ970340	CQ970340 Sequence
C 31	12.6	66.3	39	2	BD195709	BD195709 In vivo u
C 32	12.6	66.3	39	2	BD232001	BD232001 Methode a
C 33	12.6	66.3	39	2	AR282802	AR282802 Sequence
C 34	12.6	66.3	50	2	AR682667	AR682667 Sequence
C 35	12.6	66.3	60	2	CQ536153	CQ536153 Sequence
C 36	12.6	66.3	65	2	CQ557963	CQ557963 Sequence
C 37	12.4	65.3	21	2	BD194418	BD194418 Secretary
C 38	12.4	65.3	21	2	AR297198	AR297198 Sequence
C 39	12.4	65.3	24	2	CO853550	CO853550 Sequence
C 40	12.4	65.3	27	2	CO853552	CO853552 Sequence
C 41	12.4	65.3	29	2	AR614221	AR614221 Sequence
C 42	12.4	65.3	35	2	BD074489	BD074489 Genetic r
C 43	12.4	65.3	35	2	AR569451	AR569451 Sequence
C 44	12.4	65.3	35	2	AX005816	AX005816 Sequence
C 45	12.4	65.3	47	2	AR288581	AR288581 Sequence
C 46	12.4	65.3	65	2	CQ560131	CQ560131 Sequence
C 47	12.2	64.2	21	2	AR264310	AR264310 Sequence
C 48	12.2	64.2	22	2	DD191164	DD191164 Method fo
C 49	12.2	64.2	24	2	AR124725	AR124725 Sequence
C 50	12.2	64.2	26	2	BD063654	BD063654 WTI Inter
C 51	12.2	64.2	26	2	BD096366	BD096366 WTI Inter
C 52	12.2	64.2	26	2	BD103725	BD103725 A detecti
C 53	12.2	64.2	26	2	BD136223	BD136223 Method fo
C 54	12.2	64.2	26	2	BD267502	BD267502 New metal
C 55	12.2	64.2	47	2	BD134418	BD134418 Productio
C 56	12.2	64.2	47	2	AX798079	AX798079 Sequence
C 57	12.2	64.2	49	2	AX951944	AX951944 Sequence
C 58	12.2	64.2	49	2	AX952538	AX952538 Sequence
C 59	12.2	64.2	50	2	AR681411	AR681411 Sequence
C 60	12.2	64.2	60	2	CQ536042	CQ536042 Sequence
C 61	12.2	64.2	60	2	CQ540565	CQ540565 Sequence
C 62	12.2	64.2	60	2	CQ544799	CQ544799 Sequence
C 63	12.2	64.2	65	2	CQ556637	CQ556637 Sequence
C 64	12.2	64.2	67	2	AR523001	AR523001 Sequence
C 65	12.2	64.2	68	2	AR027476	AR027476 Sequence
C 66	12.2	64.2	68	2	AR082686	AR082686 Sequence
C 67	12.2	64.2	68	2	AR131323	AR131323 Sequence
C 68	12.2	64.2	70	2	DD206809	DD206809 Methods a
C 69	12.2	63.2	29	2	AR443166	AR443166 Sequence
C 70	12.2	63.2	39	2	CS120079	CS120079 Sequence
C 71	12.2	63.2	39	2	CS120295	CS120295 Sequence
C 72	12.2	63.2	41	2	AR109087	AR109087 Sequence
C 73	12.2	63.2	41	2	AR200742	AR200742 Sequence
C 74	12.2	63.2	51	2	AX483415	AX483415 Sequence
C 75	12.2	63.2	51	2	CQ007472	CQ007472 Sequence
C 76	12.2	63.2	53	2	AR590028	AR590028 Sequence
C 77	12.2	63.2	65	2	CO555655	CO555655 Sequence
C 78	11.8	62.1	16	2	A068781	A068781 reverse com
C 79	11.8	62.1	16	2	E32722	E32722 Small tripl
C 80	11.8	62.1	16	2	AX000278	AX000278 Sequence
C 81	11.8	62.1	19	2	BD080793	BD080793 Human est
C 82	11.8	62.1	19	2	BD080808	BD080808 Nove1 est
C 83	11.8	62.1	19	2	CS251594	CS251594 Sequence
C 84	11.8	62.1	20	2	A068780	A068780 Nucleotide
C 85	11.8	62.1	20	2	AR565776	AR565776 Sequence
C 86	11.8	62.1	20	2	AX009199	AX009199 Sequence
C 87	11.8	62.1	21	2	E14408	E14408 Primer. 7/1
C 88	11.8	62.1	26	2	AR078530	AR078530 Sequence
C 89	11.8	62.1	27	2	AR143841	AR143841 Sequence
C 90	11.8	62.1	27	2	BD140898	BD140898 Method fo
C 91	11.8	62.1	27	2	AR585210	AR585210 Sequence

92 11.8 62.1 31 2 AR232074
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 c 94 11.8 62.1 41 2 AX519458
 c 95 11.8 62.1 44 2 A08788
 c 96 11.8 62.1 44 2 A08788
 c 97 11.8 62.1 44 2 A08788
 c 98 11.8 62.1 44 2 A08789
 c 99 11.8 62.1 45 2 A01999
 100 11.8 62.1 45 2 A06445

ALIGNMENTS

RESULT 1
 AR451384 19 bp DNA linear PAT 20-FEB-2004
 LOCUS Sequence 29 from patent US 6673917.
 DEFINITION AR451384
 ACCESSION AR451384
 VERSION AR451384.1 GI:42682409
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.
 TITLE Antisense iAP nucleic acids and uses thereof
 JOURNAL Patent: US 6673917-A 29 06-JAN-2004;
 University of Ottawa; Ottawa;
 CAX;

FEATURES
 source 1..19
 Location/Qualifiers
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTCAC 19
 |||||
 Db 1 CGCAGCGTATCTCTTCAC 19

RESULT 2
 AX411929 19 bp DNA linear PAT 14-JUN-2002
 LOCUS Sequence 29 from Patent WO0226968.
 DEFINITION AX411929
 ACCESSION AX411929
 VERSION AX411929.1 GI:21444394
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.
 TITLE Antisense iap nucleic acids and uses thereof
 JOURNAL Patent: WO 0226968-A 29 04-APR-2002;
 University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
 Location/Qualifiers
 1..19
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="based on Homo sapiens"

FEATURES

source 1..19
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="based on Homo sapiens"

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTCAC 19

Db 1 CGCAGCGTATCTCTTCAC 19
 |||||

RESULT 3
 AR103283 23 bp DNA linear PAT 14-FEB-2001
 LOCUS Sequence 3 from patent US 6087173.
 DEFINITION AR103283
 ACCESSION AR103283
 VERSION AR103283.1 GI:12814871
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 23)
 AUTHORS Bennett, C., Frank., Ackermann, E.J. and Cowsett, L.M.
 TITLE Antisense modulation of X-linked inhibitor of apoptosis expression
 JOURNAL Patent: US 6087173-A 3 11-JUL-2000;
 Location/Qualifiers
 1..23
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 94.7%; Score 18; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCTTCAC 19
 |||||
 Db 1 GCACGGTATCTCTTCAC 18

RESULT 4
 AR559550 54 bp DNA linear PAT 08-OCT-2004
 LOCUS Sequence 5 from patent US 6750052.
 DEFINITION AR559550
 ACCESSION AR559550
 VERSION AR559550.1 GI:53969031
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 54)
 AUTHORS Shinohara, T., Singh, D. and Chylack, L.T. Jr.
 TITLE Lens epithelial cell derived growth factor
 JOURNAL Patent: US 6750052-A 5 15-JUN-2004;
 The Brigham and Women's Hospital, Inc.; Boston, MA
 Location/Qualifiers
 1..54
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 81.1%; Score 15.4; DB 2; Length 54;
 Best Local Similarity 94.1%; Pred. No. 6.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGTATCTCTTCAC 19
 |||||
 Db 48 CACGGATCTCTTCAC 32

RESULT 5
 CS027764/c 19 bp RNA linear PAT 03-MAR-2005
 LOCUS Sequence 17 from Patent WO2005014811.
 DEFINITION CS027764
 ACCESSION CS027764
 VERSION CS027764.1 GI:60497314
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.

REFERENCE 1
AUTHORS McSwiggen,J. and Chowrira,B.M.
TITLE RNA interference mediated inhibition of XIAP gene expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005014811-A 17 17-FEB-2005;
Sirta Therapeutics, Inc. (US)
FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Target Sequence/siNA sense region"

ORIGIN
Query Match 78.9%; Score 15; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCAC 19
|||||
19 CGGTATCTCCTTCAC 5

Db 19 CGGTATCTCCTTCAC 5

RESULT 6
LOCUS CS028231 19 bp RNA
DEFINITION Sequence 484 from Patent WO2005014811.
ACCESSION CS028231
VERSION CS028231.1 GI:60497781
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS McSwiggen,J. and Chowrira,B.M.
TITLE RNA interference mediated inhibition of XIAP gene expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005014811-A 484 17-FEB-2005;
Sirta Therapeutics, Inc. (US)
FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: siNA antisense region"

ORIGIN
Query Match 78.9%; Score 15; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCAC 19
|||||
1 CGGTATCTCCTTCAC 15

Db 1 CGGTATCTCCTTCAC 15

RESULT 7
LOCUS AX923594 19 bp DNA
DEFINITION Sequence 29 from Patent WO03080638.
ACCESSION AX923594
VERSION AX923594.1 GI:40216610
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Lacasse,E., Mcmann,D. and Durkin,J.P.
TITLE Antisense 1ap nucleobase oligomers and uses thereof
JOURNAL Patent: WO 03080638-A 29 02-OCT-2003;
Aegera Therapeutics Inc. (CA)

FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="based on Homo sapiens. Each nucleobase may be part of a ribonucleotide, deoxyribonucleotide, or nucleotide analog
n = T or U"

ORIGIN
Query Match 73.7%; Score 14; DB 2; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.8e+04;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCACGGTATCTCCTTCAC 19
|||||
1 CGCACGGTATCTCCTTCAC 19

Db 1 CGCACGGTATCTCCTTCAC 19

RESULT 9
LOCUS AR356378 59 bp DNA
DEFINITION Sequence 2496 from patent US 6593114.
ACCESSION AR356378
VERSION AR356378.1 GI:33762462
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 59)
AUTHORS Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and Rosen,C.A.
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 2496 15-JUL-2003;
Human Genome Sciences, Inc.; Rockville, MD
FEATURES Location/Qualifiers
source 1..59

ORIGIN /organism="unknown"
/mol_type="genomic DNA"

Query Match 72.6%; Score 13.8; DB 2; Length 59;
Best Local Similarity 88.2%; Pred. No. 5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTC 17
14 CGCAGCGATTTCTTC 30

RESULT 10 AR537934 59 bp DNA linear PAT 08-OCT-2004
LOCUS AR537934 Sequence 2496 from patent US 6737248.
DEFINITION AR537934
ACCESSION AR537934
VERSION AR537934.1 GI:53929151
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

1 (bases 1 to 59)
Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
Rosen,C.A.
Staphylococcus aureus polynucleotides and sequences
Patent: US 6737248-A 2496 18-MAY-2004;
Human Genome Sciences, Inc.; Rockville, MD
Location/Qualifiers
1..59
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 72.6%; Score 13.8; DB 2; Length 59;
Best Local Similarity 88.2%; Pred. No. 5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTC 17
14 CGCAGCGATTTCTTC 30

RESULT 11 37 bp DNA linear PAT 07-OCT-1996
LOCUS 124033
DEFINITION Sequence 15 from patent US 5541110.
ACCESSION 124033
VERSION 124033.1 GI:1603903
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

1 (bases 1 to 37)
Siegal,I.C.B.
Cloning and expression of a gene encoding bryodin 1 from Bryonia
dioica
Patent: US 5541110-A 15 30-JUL-1996;
Location/Qualifiers
1..37
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 70.5%; Score 13.4; DB 2; Length 37;
Best Local Similarity 93.3%; Pred. No. 9e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGTATCTCTTC 17
1 CATGTAATCTCTTC 15

RESULT 12

S80712 40 bp DNA linear PRI 07-MAY-1993
LOCUS S80712
DEFINITION gamma delta T cell antigen receptor delta-chain [V delta 2-J delta
1 junction] [human, peripheral blood, Genomic, 40 nt].
ACCESSION S80712
VERSION S80712.1 GI:244924

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 40)
Uyemura,K., Klotz,J., Pirmez,C., Ohmen,J., Wang,X.H., Ho,C.,
Hoffman,W.L. and Modlin,R.L.
Microanatomic clonality of gamma delta T cells in human
leishmaniasis lesions
J. Immunol. 148 (4), 1205-1211 (1992)
JOURNAL
PUBMED
REMARK
GenBank staff at the National Library of Medicine created this
entry [NCBI gbbseq 80712] from the original journal article.
Location/Qualifiers
1..40
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1..40
/gene="gamma delta T cell antigen receptor delta-chain"

ORIGIN

Query Match 70.5%; Score 13.4; DB 5; Length 40;
Best Local Similarity 93.3%; Pred. No. 8.9e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGTATCTCTTC 17
5 CACGGTATCACCCTTC 19

RESULT 13 60 bp DNA linear PAT 30-JAN-2004
LOCUS CQ541032
DEFINITION Sequence 10667 from Patent WO0210449.
ACCESSION CQ541032
VERSION CQ541032.1 GI:41507296
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL

Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Paigler,S.
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcritome
Patent: WO 0210449-A 10667 07-FEB-2002;
Compugen Inc. (US)
Location/Qualifiers
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES

SOURCE

ORIGIN

Query Match 70.5%; Score 13.4; DB 2; Length 60;
Best Local Similarity 93.3%; Pred. No. 8.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCTTCAC 19
27 CTGTATCTCTTCAC 13

```

RESULT 14
LOCUS AR311923/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2460 from patent US 6559294.
ACCESSION AR311923
VERSION AR311923.1 GI:31705349
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 20)
Griffais, R., Holseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 2460 06-MAY-2003;
Genet, S.A.;;
FRX;
FEATURES
location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 69.5%; Score 13.2; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GCACGGTATCTCTTCAC 19
Db 18 GCACGTATCTCCATCAC 1

RESULT 15
LOCUS AR721266 29 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 9 from patent US 6946294.
ACCESSION AR721266
VERSION AR721266.1 GI:77372750
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 29)
Kang, J.-G., Yun, J., Song, P.-S. and Park, C.-M.
TITLE Transgenic plant transformed with a translationally controlled
tumor protein (TCTP) gene
JOURNAL Patent: US 6946294-A 9 20-SEP-2005;
Kunho Petrochemical Co., Seoul;
KRX;
FEATURES
location/Qualifiers
source 1..29
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 69.5%; Score 13.2; DB 2; Length 29;
Best Local Similarity 83.3%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGCAGGTATCTCTTCA 18
Db 9 CGCAGTTGATCTCTTCA 26

RESULT 16
LOCUS AX925902 42 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 4 from Patent EPI352966.
ACCESSION AX925902
VERSION AX925902.1 GI:40244706
KEYWORDS

```

```

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1
Hara, Y.C., Izui, H.C., Asano, T.C., Watanabe, Y.C. and Nakamatsu
TITLE Tayoshi, C.T.
JOURNAL Method for producing L-amino acid
Patent: EP 1352966-A 4 15-OCT-2003;
Ajinomoto Co., Inc. (JP)
FEATURES
location/Qualifiers
source 1..42
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: primer"
ORIGIN
Query Match 69.5%; Score 13.2; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGCAGGTATCTCTTCA 18
Db 2 CGCAGGTATCTCTTCA 19

RESULT 17
LOCUS AR526230 56 bp DNA linear PAT 22-SEP-2004
DEFINITION Sequence 31190 from patent US 6703491.
ACCESSION AR526230
VERSION AR526230.1 GI:52461718
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 56)
Homburger, S.A., Ebens, A.J. Jr., Erickson, C.S., Francis-Lang, H.L.,
Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R.
TITLE Drosophila sequences
JOURNAL Patent: US 6703491-A 31190 09-MAR-2004;
Exelixis, Inc.; South San Francisco, CA
FEATURES
location/Qualifiers
source 1..56
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 69.5%; Score 13.2; DB 2; Length 56;
Best Local Similarity 83.3%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGCAGGTATCTCTTCA 18
Db 4 CGCAGCGCATCGCATCA 21

RESULT 18
LOCUS CO531296 65 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 931 from Patent WO0210449.
ACCESSION CO531296
VERSION CO531296.1 GI:41497560
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1
Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Paigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome

```

JOURNAL Patent: WO 0210449-A 931 07-FEB-2002;
Compugen Inc. (US)
FEATURES Location/Qualifiers
source 1..65
/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"

ORIGIN
Query Match 69.5%; Score 13.2; DB 2; Length 65;
Best Local Similarity 83.3%; Pred. No. 1e+05; 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCTTCA 18
|||||
39 CGCAAGAGATCTCTTCA 56

Db 39 CGCAAGAGATCTCTTCA 56

RESULT 19
BD074491 22 bp DNA linear PAT 27-AUG-2002
LOCUS Genetic regulation of plant growth and development.
DEFINITION BD074491 GI:22620094
ACCESSION BD074491.1 GI:22620094
VERSION JP 2001514893-A/16.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Herbert,N.P., Richards,D.E. and Pen,J.
TITLE Genetic regulation of plant growth and development
JOURNAL Patent: JP 2001514893-A 16 18-SEP-2001;
PLANT BIOSCIENCE LTD
OS Artificial Sequence
PN JP 2001514893-A/16
PD 18-SEP-2001 JP 2000509838
PF 07-AUG-1998 JP 2000509838
PI NICHOLAS PAUL HERBERT,DONALD ERNEST RICHARDS,JINLON PEN PC
C12N5/09,A01H5/00,C07K14/415,C12N1/15,C12N1/19,C12N1/21 PC
C12N5/10,C12N5/10,
PC C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N5/00 CC
Description of Artificial Sequence: Primer
FH Key Location/Qualifiers
FT source 1..22
Location/Qualifiers
1..22 /organism='Artificial Sequence'.
source Location/Qualifiers
1..22 /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 67.4%; Score 12.8; DB 2; Length 22;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGGTATCTCTTCA 19
|||||
19 AGGGTATCTGCTTCA 4

Db 19 AGGGTATCTGCTTCA 4

RESULT 20
AR569453/c 22 bp DNA linear PAT 14-DEC-2004
LOCUS AR569453
DEFINITION Sequence 27 from patent US 6762348.
ACCESSION AR569453
VERSION AR569453.1 GI:56570004
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)

AUTHORS Harberd,N.P., Richards,D.E. and Peng,J.
TITLE Genetic control of plant growth and development
JOURNAL Patent: US 6762348-A 27 13-JUL-2004;
Pioneer Hi-Bred International, Inc.; Johnston, IA;
WOX;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 67.4%; Score 12.8; DB 2; Length 22;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGGTATCTCTTCA 19
|||||
19 AGGGTATCTGCTTCA 4

Db 19 AGGGTATCTGCTTCA 4

RESULT 21
AX005818/c 22 bp DNA linear PAT 24-AUG-2000
LOCUS AX005818
DEFINITION Sequence 27 from Patent WO9909174.
ACCESSION AX005818
VERSION AX005818.1 GI:9928814
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Harberd,N.P. and Peng,J.
TITLE Genetic control of plant growth and development
JOURNAL Patent: WO 9909174-A 27 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINLON (GB)
LOCATION/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match 67.4%; Score 12.8; DB 2; Length 22;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGGTATCTCTTCA 19
|||||
19 AGGGTATCTGCTTCA 4

Db 19 AGGGTATCTGCTTCA 4

RESULT 22
BD074493 23 bp DNA linear PAT 27-AUG-2002
LOCUS BD074493
DEFINITION Genetic regulation of plant growth and development.
ACCESSION BD074493
VERSION BD074493.1 GI:22620096
KEYWORDS JP 2001514893-A/18.
SOURCE JP 2001514893-A/18.
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Herbert,N.P., Richards,D.E. and Pen,J.
TITLE Genetic regulation of plant growth and development
JOURNAL Patent: JP 2001514893-A 18 18-SEP-2001;
PLANT BIOSCIENCE LTD
OS Artificial Sequence
PN JP 2001514893-A/18
PD 18-SEP-2001 JP 2000509838
PF 07-AUG-1998 JP 2000509838
PI NICHOLAS PAUL HERBERT,DONALD ERNEST RICHARDS,JINLON PEN PC

C12N15/09,A01H5/00,C07K14/415,C12N1/15,C12N1/19,C12N1/21 PC
,C12N5/10,C12N5/10,
PC C12P21/02,C12O1/68,C12N15/00,C12N5/00,C12N5/00 CC
Description of Artificial Sequence: Primer
FH Key
FT source
1. .23
Location/Qualifiers
/organism="Artificial Sequence".
1. .23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 67.4%; Score 12.8; DB 2; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGGTATCTCCTTCAC 19
| | | | | | | | | | | | | | | | | | | | | |
4 ACGGTATCTCCTTCAC 19

Db 4 ACGGTATCTCCTTCAC 19

RESULT 23
AR569455 23 bp DNA linear PAT 14-DEC-2004
LOCUS AR569455
DEFINITION Sequence 29 from patent US 6762348.
ACCESSION AR569455
VERSION AR569455.1 GI:56570006
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Harberd,N.P., Richards,D.B. and Peng,J.
TITLE Genetic control of plant growth and development
JOURNAL Patent: US 6762348-A 29 13-JUL-2004;
Pioneer Hi-Bred International, Inc.; Johnston, IA;
WOL;
FEATURES
source Location/Qualifiers
1. .23
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 67.4%; Score 12.8; DB 2; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGGTATCTCCTTCAC 19
| | | | | | | | | | | | | | | | | | | | | |
4 ACGGTATCTCCTTCAC 19

Db 4 ACGGTATCTCCTTCAC 19

RESULT 24
AX005820 23 bp DNA linear PAT 24-AUG-2000
LOCUS AX005820
DEFINITION Sequence 29 from Patent WO9909174.
ACCESSION AX005820
VERSION AX005820.1 GI:9928816
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Harberd,N.P. and Peng,J.
TITLE Genetic control of plant growth and development
JOURNAL Patent: WO 9909174-A 29 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JIKRONG (GB)
FEATURES
source Location/Qualifiers
1. .23
/organism="synthetic construct"
/mol_type="unassigned DNA"

/db_xref="taxon:32630"
/note="Primer"

ORIGIN

Query Match 67.4%; Score 12.8; DB 2; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGGTATCTCCTTCAC 19
| | | | | | | | | | | | | | | | | | | | | |
4 ACGGTATCTCCTTCAC 19

Db 4 ACGGTATCTCCTTCAC 19

RESULT 25
AR580727/c 52 bp DNA linear PAT 15-DEC-2004
LOCUS AR580727
DEFINITION Sequence 26 from patent US 6790444.
ACCESSION AR580727
VERSION AR580727.1 GI:56611237
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52)
AUTHORS Le,J., Vilcek,J., Daddona,P., Grayeb,J., Knight,D. and Siegel,S.
TITLE Anti-TNF antibodies and peptides of human necrosis factor
JOURNAL Patent: US 6790444-A 26 14-SEP-2004;
New York University Medical Center and Centocor, Inc.; New York, NY
FEATURES
source Location/Qualifiers
1. .52
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 67.4%; Score 12.8; DB 2; Length 52;
Best Local Similarity 87.5%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGGTATCTCCTTCA 18
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27 CCCGATATCTCCTTCA 12

Db 27 CCCGATATCTCCTTCA 12

RESULT 26
BD000514 30 bp DNA linear PAT 31-JAN-2002
LOCUS BD000514
DEFINITION Method for screening G protein-coupled receptor ligand and method
ACCESSION BD000514
VERSION BD000514.1 GI:18623627
KEYWORDS JP 2000354500-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Naito,T., Saito,Y. and Morita,M.
TITLE Method for screening G protein-coupled receptor ligand and method
JOURNAL for expression cloning G protein-coupled receptor
Patent: JP 2000354500-A 2 26-DEC-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000354500-A/2
PD 26-DEC-2000
PP 12-APR-2000 JP 2000111313
PR
PI TAKAYUKI NAITO,YUTAKA SAITO,MITSUHIRO MORITA
PC C12O1/68,C07K14/47,C07K14/705,C12N5/10,C12N15/09,C12P21/02, PC
C12O1/02,
PC C12Q1/66,G01N33/15,G01N33/50,G01N33/56,G01N33/68//
PC (C12N5/10,C12R1:91), (C12N15/09,C12R1:91), (C12N5/00,C12N15/00,
PC (C12N5/00,C12R1:91), (C12N15/09,C12R1:91)
CC
FH Key Location/Qualifiers

FT source 1..30
/organism='Artificial Sequence'.
Location/Qualifiers

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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Query Match 66.3%; Score 12.6; DB 2; Length 30;
Best Local Similarity 78.9%; Pred. No. 2.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCTTCAC 19
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8 CGCAGCGTCTCTCTTCAC 26

Db

RESULT 27
DD159756 30 bp DNA linear PAT 23-NOV-2005
LOCUS
DEFINITION Method for Screening Ligands of G-Protein Coupled Receptor and
Expression Cloning Method for G-Protein Coupled Receptor.
ACCESSION DD159756
VERSION DD159756.1 GI:83959486
KEYWORDS JP 2005118050-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1 (bases 1 to 30)
Saito,Y., Naito,T. and Morita,M.
METHOD for Screening Ligands of G-Protein Coupled Receptor and
Expression Cloning Method for G-Protein Coupled Receptor
Patent: JP 2005118050-A 2 12-MAY-2005;
Japan Tobacco Inc
OS Artificial Sequence
PN JP 2005118050-A/2
PD 12-MAY-2005
PF 07-DEC-2004 JP 2004353501
PI Yutaka Saito, Takayuki Naito, Mitsuhiro Morita
CC Description of Artificial Sequence:Primer R3
FH Key Location/Qualifiers

FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCTTCAC 19
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8 CGCAGCGTCTCTCTTCAC 26

Db

RESULT 28
A06937 34 bp DNA linear PAT 04-OCT-1993
LOCUS
DEFINITION F.domesticus c-fes/fps gene, exon 1.
ACCESSION A06937
VERSION A06937.1 GI:488944
KEYWORDS
SOURCE Felis catus (cat)
ORGANISM Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
1 (bases 1 to 34)
Van de Ven,W.U.M., Roebroek,A.J.M. and Schalken,J.A.
Recombinant DNA and cDNA, mRNA, protein, antibodies, and a method

JOURNAL of detecting tumor cells
Patent: EP 0246709-A 4 25-NOV-1987;
Stichting Katholieke Universiteit
Location/Qualifiers

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source
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/mol_type="unassigned DNA"
/db_xref="taxon:9685"

ORIGIN

Query Match 66.3%; Score 12.6; DB 2; Length 34;
Best Local Similarity 78.9%; Pred. No. 2.5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCTTCAC 19
|||||
7 CGCGCGTAACTCTGCC 25

Db

RESULT 29
CQ970331 35 bp DNA linear PAT 20-DEC-2004
LOCUS
DEFINITION Sequence 2 from Patent WO2004046720.
ACCESSION CQ970331
VERSION CQ970331.1 GI:56744102
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1
Elmark,P., Furebyring,C., Ohlin,M. and Borrebaeck,C.
Methods for identifying members of specific binding pairs
Patent: WO 2004046720-A 2 03-JUN-2004;
Alligator Bioscience AB (SE)
Location/Qualifiers

FEATURES
source
1..35
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="CD40 cytoplasmic and transmembrane domain
oligonucleotide 2"

ORIGIN

Query Match 66.3%; Score 12.6; DB 2; Length 35;
Best Local Similarity 78.9%; Pred. No. 2.5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCTTCAC 19
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12 CTCACGTCTCTCTGCAC 30

Db

RESULT 30
CQ970340 35 bp DNA linear PAT 20-DEC-2004
LOCUS
DEFINITION Sequence 11 from Patent WO2004046720.
ACCESSION CQ970340
VERSION CQ970340.1 GI:56744111
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1
Elmark,P., Furebyring,C., Ohlin,M. and Borrebaeck,C.
Methods for identifying members of specific binding pairs
Patent: WO 2004046720-A 11 03-JUN-2004;
Alligator Bioscience AB (SE)
Location/Qualifiers

FEATURES
source
1..35
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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ORIGIN

Query Match 66.3%; Score 12.6; DB 2; Length 35;
 Best Local Similarity 78.9%; Pred. No. 2.5e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTCTC 19
 Db 12 CTCACCTCTCTCTCTCTC 30

RESULT 31
 BD195709/c
 LOCUS
 DEFINITION In vivo use of recombinagenic oligonucleobases to correct genetic
 lesions in hepatocytes.
 ACCESSION BD195709
 VERSION BD195709.1 GI:33005479
 KEYWORDS JP 2002511851-A/7.
 SOURCE unidentified
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 39)
 OF, R.O.T.U., Steer, C.J., Kren, B.T. and Opadhyay, P.T.B.
 In vivo use of recombinagenic oligonucleobases to correct genetic
 lesions in hepatocytes
 Patent: JP 2002511851-A 7 16-APR-2002;
 REGENTS OF THE UNIVERSITY OF MINNESOTA, CLIFFORD J STEER, BETSY T
 KREN, PARAMITA T BANDY OPADHYAY
 OS Unidentified
 PN JP 2002511851-A/7
 PD 16-APR-2002
 PR 30-APR-1998 JP 1998547429
 PR 30-APR-1997 US 60/045288, 05-AUG-1997 US 60/054837 PR
 10-NOV-1997 US 60/064996
 PI REGENTS OF THE UNIVERSITY OF MINNESOTA, CLIFFORD J STEER, BETSY
 T KREN,
 PI PARAMITA T BANDY OPADHYAY
 PC C1201/68, A61K48/00, C07H21/04
 CC Strandedness: Single;
 CC Topology: Linear;
 CC In vivo use of recombinagenic oligonucleobases to correct CC
 genetic lesions
 CC in hepatocytes
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 FT /db_xref='taxon:32644'

FEATURES
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ORIGIN

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 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTCTC 19
 Db 29 CCCCCACTATCTCTCTC 11

RESULT 32
 BD332001/c
 LOCUS
 DEFINITION Methods and compounds for the genetic treatment of hyperlipidemia.
 ACCESSION BD332001
 VERSION BD332001.1 GI:33041771
 KEYWORDS JP 2002534353-A/26.
 SOURCE unidentified
 ORGANISM unidentified

unclassified sequences.

REFERENCE 1 (bases 1 to 39)
 Steer, C.J., Kren, B.T., Hyay, P.T.B. and Chowdhury, J.R.
 Methods and compounds for the genetic treatment of hyperlipidemia
 Patent: JP 2002534353-A 26 15-OCT-2002;
 REGENTS OF THE UNIVERSITY OF MINNESOTA, ALBERT EINSTEIN COLLEGE OF
 MEDICINE OF YESHIVA UNIVERSITY
 OS R. rattus (rat)
 PN JP 2002534353-A/26
 PD 15-OCT-2002
 PR 28-AUG-1998 JP 2000531065
 PR 12-FEB-1998 US 60/074497, 30-JUN-1998 US 09/108006 PI
 CLIFFORD J STEER, BETSY T KREN, PARAMITA T BANDYOPAD HYAY, PI
 JAYANTA ROY CHOWDHURY
 PC A61K48/00, A61K9/50, A61K9/51, A61K31/71, A61K47/24, A61P9/06, PC
 C07H21/04,
 PC C12N15/09, C12N15/00
 CC Methods and compounds for the genetic treatment of CC
 hyperlipidemia
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 FT /organism='R. rattus (rat)'.
 FT location/Qualifiers
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 FT /organism='unidentified'
 FT /mol_type='genomic DNA'
 FT /db_xref='taxon:32644'

FEATURES
 source

ORIGIN

Query Match 66.3%; Score 12.6; DB 2; Length 39;
 Best Local Similarity 78.9%; Pred. No. 2.5e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTCTC 19
 Db 29 CCCCCACTATCTCTCTC 11

RESULT 33
 AR282802/c
 LOCUS
 DEFINITION Sequence 33 from patent US 6524613.
 ACCESSION AR282802
 VERSION AR282802.1 GI:29719586
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 39)
 Steer, C.J., Kren, B.T., Bandyopadhyay, P. and Roy-Chowdhury, J.
 Hepatocellular chimeraplasty
 Patent: US 6524613-A 33 25-FEB-2003;
 Regents of the University of Minnesota and Yeshiva University;
 Minneapolis, MN
 location/Qualifiers
 1..39
 /organism="unknown"
 /mol_type="genomic DNA"

FEATURES
 source

ORIGIN

Query Match 66.3%; Score 12.6; DB 2; Length 39;
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 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTCTC 19
 Db 29 CCCCCACTATCTCTCTC 11

RESULT 34
 AR682667/c
 LOCUS
 DEFINITION Sequence 2096 from patent US 6905827.
 ACCESSION AR682667

unclassified sequences.

VERSION AR682667.1 GI:74464437
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wohlgenuth,J., Fry,K., Woodward,R. and Ly,N.
TITLE Methods and compositions for diagnosing or monitoring auto immune
and chronic inflammatory diseases
JOURNAL Patent: US 6905827-A 2006 14-JUN-2005;
Expression Diagnostics, Inc.; So. San Francisco, CA
FEATURES
source 1..50
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 66.3%; Score 12.6; DB 2; Length 50;
Best Local Similarity 78.9%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGCAGCGTATCTCTCTCAC 19
DB 49 CTCACGTCTCTCTCTCAC 31
RESULT 35
LOCUS COS36153 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 5788 from Patent WO0210449.
ACCESSION COS36153
VERSION COS36153.1 GI:41502417
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variance that populate a transcritpome
JOURNAL Patent: WO 0210449-A 5788 07-FEB-2002;
Compugen Inc. (US)
FEATURES
source 1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
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Best Local Similarity 78.9%; Pred. No. 2.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGCAGCGTATCTCTCTCAC 19
DB 25 CCCACGATATCTGCTCAC 43
RESULT 36
LOCUS COS57963/c 65 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 27598 from Patent WO0210449.
ACCESSION COS57963
VERSION COS57963.1 GI:41524390
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
ACCESSION AR297198

AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcritpome
JOURNAL Patent: WO 0210449-A 27598 07-FEB-2002;
Compugen Inc. (US)
FEATURES
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/organism="Mus musculus"
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Query Match 66.3%; Score 12.6; DB 2; Length 65;
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Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGCAGCGTATCTCTCTCAC 19
DB 40 CGCAGCGATCTCTCTCTC 22
RESULT 37
LOCUS BD194418 21 bp DNA linear PAT 17-JUL-2003
DEFINITION Secretory proteins and polynucleotides encoding the same.
ACCESSION BD194418
VERSION BD194418.1 GI:33004159
KEYWORDS JP 2002509722-A/13.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A.C., Evans,C.,
Merberg,D., Treacy,M., Agostino,M.J. and Li,R.J.S.
TITLE Secretory proteins and polynucleotides encoding the same
JOURNAL Patent: JP 2002509722-A 13 02-APR-2002;
GENETICS INSTITUTE INC
COMMENT OS Artificial Sequence
PN JP 2002509722-A/13
PD 02-APR-2002
PF 30-MAR-1999 JP 2000541293
PR 31-MAR-1998 US 60/080110, 29-MAR-1999 US 09/280591 PI
KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A COLUINS PI
RACIE,
PI CHERYL EVANS,DAVID MERBERG,MAURICE TREACY,MICHAEL J AGOSTINO,
PI ROBERT J STEININGER II
PC C12N15/09,C07K7/00,C07K14/00,C07K14/435,C12N5/10,C12N15/00, PC
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CC Oligonucleotide
FH key
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Best Local Similarity 92.9%; Pred. No. 3.6e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 CACGCTATCTCTT 16
DB 5 CACTGTATCTCTT 18
RESULT 38
LOCUS AR297198 21 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 8933 from patent US 6537751.
ACCESSION AR297198

VERSION AR297198.1 GI:31684482
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
Patent: US 6537751-A 8933 25-MAR-2003;
Genet S.A.;;
FRX;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 ACGGTATCTCCTTC 17
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7 ACTGTATCTCCTTC 20
Db
RESULT 39
CQ853550 24 bp DNA linear PAT 23-AUG-2004
LOCUS
DEFINITION Sequence 15 from Patent WO2004067570.
ACCESSION CQ853550
VERSION CQ853550.1 GI:51509753
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Cuellar, C., Saragovi, U., du Ruisseau, P., Gold, P., Bernard, N. and
Moffett, S.
TITLE Prostate cancer diagnosis and treatment
JOURNAL Patent: WO 2004067570-A 15 12-AUG-2004;
Proscan RX Pharma (CA)
FEATURES Location/Qualifiers
source 1..24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Primer"
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Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 GGATCTCCTTCAC 19
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5 GGAATCTCCTTCAC 18
Db
RESULT 40
CQ853552 27 bp DNA linear PAT 23-AUG-2004
LOCUS
DEFINITION Sequence 17 from Patent WO2004067570.
ACCESSION CQ853552
VERSION CQ853552.1 GI:51509755
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Cuellar, C., Saragovi, U., du Ruisseau, P., Gold, P., Bernard, N. and
Moffett, S.

TITLE Prostate cancer diagnosis and treatment
JOURNAL Patent: WO 2004067570-A 17 12-AUG-2004;
Proscan RX Pharma (CA)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Primer"
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Best Local Similarity 92.9%; Pred. No. 3.4e+05;
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QY 6 GGATCTCCTTCAC 19
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13 GGAATCTCCTTCAC 26
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 08:42:32 ; Search time 99.3333 Seconds
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Title: US-10-636-065-29

Perfect score: 19

Sequence: 1 cgcacggatcccttcac 19

Scoring table: IDENTITY NUC

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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 40218

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Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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- 1: Issued Patents NA.*
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- 3: /EMC_Celerra_SIDS3/prodata/2/ina/5 COMB.seq.*
- 4: /EMC_Celerra_SIDS3/prodata/2/ina/6 COMB.seq.*
- 5: /EMC_Celerra_SIDS3/prodata/2/ina/7 COMB.seq.*
- 6: /EMC_Celerra_SIDS3/prodata/2/ina/H COMB.seq.*
- 7: /EMC_Celerra_SIDS3/prodata/2/ina/PTUS COMB.seq.*
- 8: /EMC_Celerra_SIDS3/prodata/2/ina/PT COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	19	100.0	19	3	US-09-672-717-29
2	11	57.9	19	3	US-09-422-978-7559
3	10.8	56.8	19	3	US-09-696-791-3034
4	10.8	56.8	19	3	US-09-696-791-3128
5	10.8	56.8	19	3	US-09-696-791-3129
6	10.8	56.8	19	3	US-09-696-791-3130
7	10.8	56.8	19	3	US-09-696-791-3131
8	10.6	55.8	19	3	US-09-422-978-9324
9	10.4	54.7	19	3	US-09-422-978-9940
10	10.4	54.7	19	3	US-09-422-978-6219
11	10.4	54.7	19	3	US-09-938-077-18
12	10.4	54.7	19	3	US-09-696-791-3132
13	10	52.6	19	2	US-08-182-619-2
14	10	52.6	19	2	US-08-330-535A-2
15	10	52.6	19	2	US-08-838-844-2
16	10	52.6	19	3	US-08-851-350-26
17	10	52.6	19	3	US-08-924-287A-26
18	9.8	51.6	19	2	US-08-117-952-739
19	9.8	51.6	19	2	US-08-549-004A-3
20	9.8	51.6	19	3	US-09-051-862A-3
21	9.8	51.6	19	3	US-08-815-795-2
22	9.8	51.6	19	3	US-09-422-978-5993
23	9.8	51.6	19	3	US-10-130-158A-9

C 24	9.8	51.6	19	3	US-10-130-158A-10	Sequence 10, Appl
C 25	9.6	50.5	19	3	US-09-108-006C-28	Sequence 28, Appl
C 26	9.6	50.5	19	3	US-09-422-978-7112	Sequence 7112, Ap
C 27	9.6	50.5	19	3	US-09-688-188B-74	Sequence 74, Appl
C 28	9.6	50.5	19	3	US-09-291-417D-74	Sequence 74, Appl
C 29	9.6	50.5	19	3	US-09-544-398B-169	Sequence 169, App
C 30	9.6	50.5	19	3	US-09-543-771B-169	Sequence 169, App
C 31	9.6	50.5	19	5	US-10-032-495A-20	Sequence 20, Appl
C 32	9.4	49.5	19	3	US-09-696-791-3133	Sequence 3133, Ap
C 33	9.4	49.5	19	3	US-09-747-385-7	Sequence 7, Appl1
C 34	9.2	48.4	19	3	US-09-506-729-1	Sequence 1, Appl1
C 35	9.2	48.4	19	3	US-09-422-978-5154	Sequence 5154, Ap
C 36	9.2	48.4	19	3	US-09-973-132-2	Sequence 2, Appl1
C 37	9.2	48.4	19	3	US-09-696-791-1137	Sequence 1137, Ap
C 38	9.2	48.4	19	3	US-09-696-791-1138	Sequence 1138, Ap
C 39	9.2	48.4	19	3	US-09-696-791-1429	Sequence 1429, Ap
C 40	9.2	48.4	19	3	US-09-696-791-1430	Sequence 1430, Ap
C 41	9.2	48.4	19	10	5217865-10	Patent No. 5217865
C 42	9.2	48.4	19	10	5475095-10	Patent No. 5475095
C 43	9.2	47.4	19	2	US-08-086-915-9	Sequence 9, Appl1
C 44	9.2	47.4	19	2	US-08-769-601-3	Sequence 3, Appl1
C 45	9.2	47.4	19	2	US-08-825-558-9	Sequence 9, Appl1
C 46	9.2	47.4	19	3	US-08-300-928C-34	Sequence 34, Appl
C 47	9.2	47.4	19	3	US-08-430-944D-34	Sequence 34, Appl
C 48	9.2	47.4	19	3	US-08-430-014-34	Sequence 34, Appl
C 49	9.2	47.4	19	3	US-08-431-184-34	Sequence 34, Appl
C 50	9.2	47.4	19	3	US-08-836-352A-9	Sequence 9, Appl1
C 51	9.2	47.4	19	3	US-09-338-907-554	Sequence 554, App
C 52	9.2	47.4	19	3	US-09-218-207-554	Sequence 5, Appl1
C 53	9.2	47.4	19	3	US-09-312-611-9	Sequence 9, Appl1
C 54	9.2	47.4	19	3	US-09-422-978-4426	Sequence 4426, Ap
C 55	9.2	47.4	19	3	US-09-696-791-2439	Sequence 2439, Ap
C 56	9.2	47.4	19	3	US-09-696-791-2946	Sequence 2946, Ap
C 57	9.2	47.4	19	5	US-10-258-828-3	Sequence 3, Appl1
C 58	9.2	46.3	19	2	US-07-767-135-4	Sequence 4, Appl1
C 59	9.2	46.3	19	2	US-08-190-711-1	Sequence 1, Appl1
C 60	9.2	46.3	19	2	US-08-241-853-34	Sequence 34, Appl
C 61	9.2	46.3	19	2	US-08-433-854-49	Sequence 49, Appl
C 62	9.2	46.3	19	2	US-08-174-745A-49	Sequence 49, Appl
C 63	9.2	46.3	19	2	US-08-246-583-13	Sequence 13, Appl
C 64	9.2	46.3	19	2	US-08-132-168B-6	Sequence 6, Appl1
C 65	9.2	46.3	19	2	US-08-399-986B-19	Sequence 19, Appl
C 66	9.2	46.3	19	2	US-08-493-754A-19	Sequence 19, Appl
C 67	9.2	46.3	19	2	US-08-195-947-49	Sequence 49, Appl
C 68	9.2	46.3	19	2	US-08-850-917-34	Sequence 34, Appl
C 69	9.2	46.3	19	2	US-08-450-905B-77	Sequence 77, Appl
C 70	9.2	46.3	19	2	US-08-433-885-49	Sequence 49, Appl
C 71	9.2	46.3	19	2	US-08-951-648-10	Sequence 10, Appl
C 72	9.2	46.3	19	2	US-08-433-908B-49	Sequence 49, Appl
C 73	9.2	46.3	19	3	US-07-982-759F-77	Sequence 77, Appl
C 74	9.2	46.3	19	3	US-09-338-907-495	Sequence 495, App
C 75	9.2	46.3	19	3	US-08-410-614-49	Sequence 49, Appl
C 76	9.2	46.3	19	3	US-09-218-207-495	Sequence 495, App
C 77	9.2	46.3	19	3	US-09-328-750A-6	Sequence 6, Appl1
C 78	9.2	46.3	19	3	US-09-636-791A-24	Sequence 24, Appl
C 79	9.2	46.3	19	3	US-09-422-978-5152	Sequence 5152, Ap
C 80	9.2	46.3	19	3	US-09-422-978-7626	Sequence 7626, Ap
C 81	9.2	46.3	19	3	US-09-696-791-1136	Sequence 1136, Ap
C 82	9.2	46.3	19	3	US-09-696-791-1591	Sequence 1591, Ap
C 83	9.2	46.3	19	3	US-09-696-791-1592	Sequence 1592, Ap
C 84	9.2	46.3	19	3	US-08-444-994-1	Sequence 1, Appl
C 85	9.2	46.3	19	2	US-08-244-189-4	Sequence 4, Appl1
C 86	9.2	46.3	19	2	US-08-452-262-12	Sequence 12, Appl
C 87	9.2	46.3	19	2	US-08-734-550-12	Sequence 12, Appl
C 88	9.2	46.3	19	2	US-08-656-586-10	Sequence 10, Appl
C 89	9.2	46.3	19	3	US-09-138-024-1	Sequence 1, Appl1
C 90	9.2	46.3	19	3	US-08-881-784-38	Sequence 38, Appl
C 91	9.2	46.3	19	3	US-09-292-768-39	Sequence 39, Appl
C 92	9.2	46.3	19	3	US-09-522-800-7	Sequence 7, Appl1
C 93	9.2	46.3	19	3	US-09-103-875-111	Sequence 111, App
C 94	9.2	46.3	19	3	US-09-037-990B-78	Sequence 78, Appl
C 95	9.2	46.3	19	3	US-08-637-732A-29	Sequence 29, Appl
C 96	9.2	46.3	19	3	US-09-504-358-36	Sequence 36, Appl

C 97	8.6	45.3	19	3	US-09-104-066-1	Sequence 1, Appl1	170	8.4	44.2	19	3	US-09-902-563-41	Sequence 41, Appl1
C 98	8.6	45.3	19	3	US-09-531-000-70	Sequence 70, Appl	171	8.4	44.2	19	3	US-10-176-255-12	Sequence 12, Appl
C 99	8.6	45.3	19	3	US-09-954-314-36	Sequence 36, Appl	172	8.4	44.2	19	3	US-10-197-288B-11	Sequence 31, Appl
C 100	8.6	45.3	19	3	US-08-820-479-6	Sequence 6, Appl1	C 173	8.4	44.2	19	3	US-10-071-179-107	Sequence 107, App
C 101	8.6	45.3	19	3	US-09-573-322-1	Sequence 1, Appl1	C 174	8.4	44.2	19	3	US-09-693-333-144	Sequence 144, App
C 102	8.6	45.3	19	3	US-09-422-978-5002	Sequence 5002, Ap	C 175	8.4	44.2	19	3	US-09-697-123B-25	Sequence 25, Appl
C 103	8.6	45.3	19	3	US-09-747-391-240	Sequence 240, Appl	C 176	8.4	44.2	19	3	US-10-928-327A-6	Sequence 6, Appl1
C 104	8.6	45.3	19	3	US-09-358-321C-52	Sequence 52, Appl	C 177	8.4	44.2	19	4	US-10-428-826-111	Sequence 141, App
C 105	8.6	45.3	19	3	US-09-696-791-174	Sequence 174, Appl	C 178	8.4	44.2	19	5	US-10-033-495A-9	Sequence 9, Appl1
C 106	8.6	45.3	19	3	US-09-696-791-1018	Sequence 1018, Ap	C 179	8.4	44.2	19	7	PCT-US95-08605-11	Sequence 11, Appl
C 107	8.6	45.3	19	3	US-09-696-791-1019	Sequence 1019, Ap	C 180	8.2	43.2	19	2	US-08-110-294A-44	Sequence 44, Appl
C 108	8.6	45.3	19	3	US-09-696-791-1020	Sequence 1020, Ap	C 181	8.2	43.2	19	2	US-08-389-926-44	Sequence 44, Appl
C 109	8.6	45.3	19	3	US-10-330-562-36	Sequence 36, Appl	C 182	8.2	43.2	19	2	US-08-532-727A-6	Sequence 6, Appl1
C 110	8.6	45.3	19	3	US-09-959-120B-26	Sequence 26, Appl	C 183	8.2	43.2	19	2	US-08-743-637B-68	Sequence 68, Appl
C 111	8.6	45.3	19	7	PCT-US94-06331A-3	Sequence 3, Appl1	C 184	8.2	43.2	19	3	US-08-526-840B-68	Sequence 68, Appl
C 112	8.6	45.3	19	7	PCT-US96-07528-12	Sequence 12, Appl	C 185	8.2	43.2	19	3	US-08-960-760-84	Sequence 84, Appl
C 113	8.4	44.2	19	2	US-08-388-381-11	Sequence 11, Appl	C 186	8.2	43.2	19	3	US-08-960-760-122	Sequence 122, App
C 114	8.4	44.2	19	2	US-08-420-244-3	Sequence 3, Appl1	C 187	8.2	43.2	19	3	US-09-311-260-63	Sequence 63, Appl
C 115	8.4	44.2	19	2	US-08-166-664-14	Sequence 14, Appl	C 188	8.2	43.2	19	3	US-09-518-727A-6	Sequence 84, Appl
C 116	8.4	44.2	19	2	US-08-313-185-19	Sequence 19, Appl	C 189	8.2	43.2	19	3	US-09-073-898-84	Sequence 122, App
C 117	8.4	44.2	19	2	US-08-849-536A-7	Sequence 7, Appl1	C 190	8.2	43.2	19	3	US-09-338-907-473	Sequence 473, App
C 118	8.4	44.2	19	3	US-08-765-626-11	Sequence 11, Appl	C 191	8.2	43.2	19	3	US-09-338-907-488	Sequence 488, App
C 119	8.4	44.2	19	3	US-09-292-071-12	Sequence 12, Appl	C 192	8.2	43.2	19	3	US-08-797-358B-5	Sequence 5, Appl1
C 120	8.4	44.2	19	3	US-09-082-614A-19	Sequence 19, Appl	C 193	8.2	43.2	19	3	US-09-218-207-473	Sequence 473, App
C 121	8.4	44.2	19	3	US-09-932-069A-12	Sequence 12, Appl	C 194	8.2	43.2	19	3	US-09-218-207-488	Sequence 488, App
C 122	8.4	44.2	19	3	US-09-418-721-12	Sequence 12, Appl	C 195	8.2	43.2	19	3	US-09-561-989-6	Sequence 6, Appl1
C 123	8.4	44.2	19	3	US-09-050-159-112	Sequence 112, App	C 196	8.2	43.2	19	3	US-09-422-978-4088	Sequence 4088, Ap
C 124	8.4	44.2	19	3	US-09-050-159-114	Sequence 114, App	C 197	8.2	43.2	19	3	US-09-422-978-6464	Sequence 6464, Ap
C 125	8.4	44.2	19	3	US-09-061-769A-9	Sequence 9, Appl1	C 198	8.2	43.2	19	3	US-09-422-978-7129	Sequence 7129, Ap
C 126	8.4	44.2	19	3	US-08-478-316-93	Sequence 93, Appl	C 199	8.2	43.2	19	3	US-09-556-377A-10	Sequence 10, Appl
C 127	8.4	44.2	19	3	US-09-338-907-395	Sequence 395, App	C 200	8.2	43.2	19	3	US-09-526-193A-135	Sequence 135, App
C 128	8.4	44.2	19	3	US-09-218-207-395	Sequence 395, App	C 201	8.2	43.2	19	3	US-09-982-212-40	Sequence 40, Appl
C 129	8.4	44.2	19	3	US-09-534-407-20	Sequence 20, Appl	C 202	8.2	43.2	19	3	US-09-850-351A-84	Sequence 84, Appl
C 130	8.4	44.2	19	3	US-08-420-672-13	Sequence 13, Appl	C 203	8.2	43.2	19	3	US-09-850-351A-122	Sequence 122, App
C 131	8.4	44.2	19	3	US-09-019-793A-93	Sequence 93, Appl	C 204	8.2	43.2	19	3	US-09-747-391-50	Sequence 50, Appl
C 132	8.4	44.2	19	3	US-09-345-082-107	Sequence 107, App	C 205	8.2	43.2	19	3	US-09-747-391-51	Sequence 51, Appl
C 133	8.4	44.2	19	3	US-09-442-143A-41	Sequence 41, Appl	C 206	8.2	43.2	19	3	US-09-747-391-130	Sequence 130, App
C 134	8.4	44.2	19	3	US-09-387-341-199	Sequence 199, App	C 207	8.2	43.2	19	3	US-09-747-391-135	Sequence 135, App
C 135	8.4	44.2	19	3	US-09-328-750A-7	Sequence 7, Appl1	C 208	8.2	43.2	19	3	US-08-401-192-3	Sequence 3, Appl1
C 136	8.4	44.2	19	3	US-09-767-013-12	Sequence 12, Appl	C 209	8.2	43.2	19	3	US-09-696-791-175	Sequence 175, App
C 137	8.4	44.2	19	3	US-09-545-686-31	Sequence 31, Appl	C 210	8.2	43.2	19	3	US-09-696-791-1139	Sequence 1139, Ap
C 138	8.4	44.2	19	3	US-09-475-947A-99	Sequence 99, Appl	C 211	8.2	43.2	19	3	US-09-696-791-1431	Sequence 1431, Ap
C 139	8.4	44.2	19	3	US-09-775-947A-100	Sequence 100, App	C 212	8.2	43.2	19	3	US-09-696-791-1721	Sequence 1721, Ap
C 140	8.4	44.2	19	3	US-09-588-995A-85	Sequence 117, App	C 213	8.2	43.2	19	3	US-09-696-791-1722	Sequence 1722, Ap
C 141	8.4	44.2	19	3	US-09-958-995A-85	Sequence 85, Appl	C 214	8.2	43.2	19	3	US-09-696-791-1123	Sequence 1123, Ap
C 142	8.4	44.2	19	3	US-09-999-201B-20	Sequence 20, Appl	C 215	8.2	43.2	19	3	US-09-696-791-1830	Sequence 1830, Ap
C 143	8.4	44.2	19	3	US-09-422-978-3958	Sequence 3958, Ap	C 216	8.2	43.2	19	3	US-09-696-791-2254	Sequence 2254, Ap
C 144	8.4	44.2	19	3	US-09-422-978-4936	Sequence 4936, Ap	C 217	8.2	43.2	19	3	US-09-696-791-2255	Sequence 2255, Ap
C 145	8.4	44.2	19	3	US-09-422-978-6771	Sequence 6771, Ap	C 218	8.2	43.2	19	3	US-09-696-791-2256	Sequence 2256, Ap
C 146	8.4	44.2	19	3	US-09-422-978-6995	Sequence 6995, Ap	C 219	8.2	43.2	19	3	US-09-696-791-3042	Sequence 3042, Ap
C 147	8.4	44.2	19	3	US-09-422-978-7741	Sequence 7741, Ap	C 220	8.2	43.2	19	3	US-09-696-791-3043	Sequence 3043, Ap
C 148	8.4	44.2	19	3	US-09-422-978-10354	Sequence 10354, A	C 221	8.2	43.2	19	3	US-09-696-791-1044	Sequence 3044, Ap
C 149	8.4	44.2	19	3	US-09-422-978-11231	Sequence 11231, A	C 222	8.2	43.2	19	3	US-09-073-881-11	Sequence 11, Appl
C 150	8.4	44.2	19	3	US-09-422-978-1168	Sequence 1168, A	C 223	8.2	43.2	19	3	US-10-131-827-8825	Sequence 8825, Ap
C 151	8.4	44.2	19	3	US-09-392-072-12	Sequence 12, Appl	C 224	8.2	43.2	19	4	US-09-977-868-40	Sequence 40, Appl
C 152	8.4	44.2	19	3	US-09-908-500A-22	Sequence 22, Appl	C 225	8.2	43.2	19	5	US-10-131-831-8825	Sequence 8825, Ap
C 153	8.4	44.2	19	3	US-09-747-391-16	Sequence 16, Appl	C 226	8.2	43.2	19	5	US-10-033-495A-24	Sequence 24, Appl
C 154	8.4	44.2	19	3	US-10-281-673A-20	Sequence 20, Appl	C 227	8.2	43.2	19	2	US-08-127-954-23	Sequence 23, Appl
C 155	8.4	44.2	19	3	US-08-401-192-4	Sequence 4, Appl1	C 228	8	42.1	19	2	US-08-152-482-5	Sequence 5, Appl1
C 156	8.4	44.2	19	3	US-09-696-791-449	Sequence 449, App	C 229	8	42.1	19	2	US-08-748-591-21	Sequence 21, Appl
C 157	8.4	44.2	19	3	US-09-696-791-450	Sequence 450, App	C 230	8	42.1	19	2	US-08-779-341-5	Sequence 5, Appl1
C 158	8.4	44.2	19	3	US-09-696-791-451	Sequence 451, App	C 231	8	42.1	19	2	US-08-544-577-5	Sequence 5, Appl1
C 159	8.4	44.2	19	3	US-09-696-791-452	Sequence 452, App	C 232	8	42.1	19	2	US-08-833-883-17	Sequence 17, Appl
C 160	8.4	44.2	19	3	US-09-696-791-453	Sequence 453, App	C 233	8	42.1	19	2	US-08-833-883-37	Sequence 37, Appl
C 161	8.4	44.2	19	3	US-09-696-791-454	Sequence 454, App	C 234	8	42.1	19	2	US-08-444-461D-2	Sequence 2, Appl1
C 162	8.4	44.2	19	3	US-09-696-791-455	Sequence 455, App	C 235	8	42.1	19	2	US-08-833-877-17	Sequence 17, Appl
C 163	8.4	44.2	19	3	US-09-696-791-1274	Sequence 1274, Ap	C 236	8	42.1	19	2	US-08-833-877-37	Sequence 37, Appl
C 164	8.4	44.2	19	3	US-09-696-791-1275	Sequence 1275, Ap	C 237	8	42.1	19	2	US-08-779-342-5	Sequence 5, Appl1
C 165	8.4	44.2	19	3	US-09-696-791-1276	Sequence 1276, Ap	C 238	8	42.1	19	2	US-08-282-197C-3	Sequence 3, Appl1
C 166	8.4	44.2	19	3	US-09-696-791-1898	Sequence 1898, Ap	C 239	8	42.1	19	3	US-08-665-259-53	Sequence 53, Appl1
C 167	8.4	44.2	19	3	US-09-696-791-2116	Sequence 2116, Ap	C 240	8	42.1	19	3	US-09-035-190-5	Sequence 5, Appl1
C 168	8.4	44.2	19	3	US-09-696-791-3142	Sequence 3142, Ap	C 241	8	42.1	19	3	US-08-762-500-53	Sequence 53, Appl1
C 169	8.4	44.2	19	3	US-09-601-326-141	Sequence 141, App	C 242	8	42.1	19	3	US-08-895-707-19	Sequence 19, Appl

C 243	8	42.1	19	3	US-09-191-099-13	Sequence 13, Appl	316	7.8	41.1	19	2	US-08-440-740A-43	Sequence 43, Appl
244	8	42.1	19	3	US-09-108-099-5	Sequence 5, Appl	C 317	7.8	41.1	19	2	US-08-223-355-14	Sequence 14, Appl
245	8	42.1	19	3	US-09-108-100-5	Sequence 5, Appl	C 318	7.8	41.1	19	2	US-09-097-562-13	Sequence 3, Appl
C 246	8	42.1	19	3	US-09-407-818-10	Sequence 10, Appl	319	7.8	41.1	19	2	US-08-344-155C-43	Sequence 43, Appl
C 247	8	42.1	19	3	US-08-943-571-7	Sequence 7, Appl	C 320	7.8	41.1	19	2	US-08-696-900-2	Sequence 2, Appl
248	8	42.1	19	3	US-09-316-349-5	Sequence 4, Appl	321	7.8	41.1	19	2	US-08-955-138-39	Sequence 39, Appl
249	8	42.1	19	3	US-09-115-475-4	Sequence 4, Appl	322	7.8	41.1	19	3	US-08-982-845B-13	Sequence 43, Appl
C 250	8	42.1	19	3	US-09-387-341-198	Sequence 198, Appl	C 323	7.8	41.1	19	3	US-08-445-643B-18	Sequence 18, Appl
C 251	8	42.1	19	3	US-09-661-711A-23	Sequence 23, Appl	C 324	7.8	41.1	19	3	US-08-445-644C-18	Sequence 18, Appl
C 252	8	42.1	19	3	US-09-422-978-5106	Sequence 5106, Ap	325	7.8	41.1	19	3	US-08-991-525B-43	Sequence 43, Appl
C 253	8	42.1	19	3	US-09-422-978-5969	Sequence 6969, Ap	326	7.8	41.1	19	3	US-09-085-759-43	Sequence 43, Appl
C 254	8	42.1	19	3	US-09-422-978-7989	Sequence 7989, Ap	327	7.8	41.1	19	3	US-09-128-996-43	Sequence 43, Appl
255	8	42.1	19	3	US-09-422-978-10081	Sequence 10081, A	C 328	7.8	41.1	19	3	US-09-192-657B-10	Sequence 10, Appl
256	8	42.1	19	3	US-09-422-978-11399	Sequence 11399, A	C 329	7.8	41.1	19	3	US-09-192-657B-14	Sequence 14, Appl
257	8	42.1	19	3	US-09-650-229-5	Sequence 5, Appl	C 330	7.8	41.1	19	3	US-09-342-479-2	Sequence 2, Appl
C 258	8	42.1	19	3	US-09-982-212-34	Sequence 34, Appl	C 331	7.8	41.1	19	3	US-09-300-672-16	Sequence 16, Appl
C 259	8	42.1	19	3	US-09-261-104-12	Sequence 12, Appl	332	7.8	41.1	19	3	US-09-117-525-9	Sequence 9, Appl
260	8	42.1	19	3	US-09-796-081-1	Sequence 1, Appl	333	7.8	41.1	19	3	US-09-009-490A-43	Sequence 43, Appl
C 261	8	42.1	19	3	US-09-796-081-2	Sequence 2, Appl	334	7.8	41.1	19	3	US-09-468-738A-15	Sequence 15, Appl
262	8	42.1	19	3	US-09-630-202-5	Sequence 5, Appl	335	7.8	41.1	19	3	US-09-326-186B-98	Sequence 98, Appl
263	8	42.1	19	3	US-09-688-078-18	Sequence 18, Appl	C 336	7.8	41.1	19	3	US-09-563-826-5	Sequence 5, Appl
264	8	42.1	19	3	US-09-672-717-37	Sequence 37, Appl	C 337	7.8	41.1	19	3	US-09-504-358-46	Sequence 46, Appl
265	8	42.1	19	3	US-09-032-438C-23	Sequence 23, Appl	C 338	7.8	41.1	19	3	US-09-395-345-30	Sequence 30, Appl
C 266	8	42.1	19	3	US-08-983-605-55	Sequence 55, Appl	339	7.8	41.1	19	3	US-09-513-007-6	Sequence 6, Appl
C 267	8	42.1	19	3	US-09-696-791-526	Sequence 526, Ap	340	7.8	41.1	19	3	US-09-940-019-15	Sequence 15, Appl
268	8	42.1	19	3	US-09-696-791-1277	Sequence 1277, Ap	341	7.8	41.1	19	3	US-09-555-889A-5	Sequence 5, Appl
269	8	42.1	19	3	US-09-696-791-1278	Sequence 1278, Ap	C 342	7.8	41.1	19	3	US-09-434-408-16	Sequence 16, Appl
270	8	42.1	19	3	US-09-696-791-1279	Sequence 1281, Ap	C 343	7.8	41.1	19	3	US-08-044-8570-18	Sequence 18, Appl
271	8	42.1	19	3	US-09-696-791-1280	Sequence 1282, Ap	344	7.8	41.1	19	3	US-09-954-314-46	Sequence 46, Appl
272	8	42.1	19	3	US-09-696-791-1682	Sequence 2680, Ap	345	7.8	41.1	19	3	US-09-940-037A-15	Sequence 15, Appl
273	8	42.1	19	3	US-09-696-791-2681	Sequence 2681, Ap	346	7.8	41.1	19	3	US-09-540-257B-22	Sequence 22, Appl
274	8	42.1	19	3	US-09-696-791-2682	Sequence 2682, Ap	347	7.8	41.1	19	3	US-09-649-747-83	Sequence 83, Appl
275	8	42.1	19	3	US-09-696-791-2683	Sequence 2683, Ap	C 348	7.8	41.1	19	3	US-09-422-978-3954	Sequence 3954, Ap
276	8	42.1	19	3	US-09-696-791-3148	Sequence 3148, Ap	C 349	7.8	41.1	19	3	US-09-422-978-4067	Sequence 4067, Ap
277	8	42.1	19	3	US-09-696-791-3149	Sequence 3150, Ap	C 350	7.8	41.1	19	3	US-09-422-978-4831	Sequence 4832, Ap
278	8	42.1	19	3	US-09-696-791-3150	Sequence 3151, Ap	C 351	7.8	41.1	19	3	US-09-422-978-5785	Sequence 5785, Ap
279	8	42.1	19	3	US-09-696-791-3151	Sequence 3152, Ap	352	7.8	41.1	19	3	US-09-422-978-6717	Sequence 6717, Ap
280	8	42.1	19	3	US-09-696-791-3152	Sequence 3508, Ap	353	7.8	41.1	19	3	US-09-422-978-8141	Sequence 8141, Ap
281	8	42.1	19	3	US-09-696-791-3508	Sequence 8, Appl	C 354	7.8	41.1	19	3	US-09-422-978-8368	Sequence 8368, Ap
C 282	8	42.1	19	3	US-09-720-435A-8	Sequence 8, Appl	C 355	7.8	41.1	19	3	US-09-422-978-8368	Sequence 8368, Ap
C 283	8	42.1	19	3	US-09-720-435A-13	Sequence 13, Appl	356	7.8	41.1	19	3	US-09-422-978-8368	Sequence 10581, A
C 284	8	42.1	19	3	US-09-269-446D-74	Sequence 16, Appl	C 357	7.8	41.1	19	3	US-09-422-978-10583	Sequence 10, Appl
285	8	42.1	19	3	US-09-479-040-18	Sequence 3, Appl	C 358	7.8	41.1	19	3	US-09-356-806-100	Sequence 100, Appl
286	8	42.1	19	3	US-09-984-037-3	Sequence 14, Appl	C 359	7.8	41.1	19	3	US-09-356-806-101	Sequence 28, Appl
287	8	42.1	19	3	US-09-959-716-14	Sequence 10, Appl	C 360	7.8	41.1	19	3	US-09-831-642-10	Sequence 241, Appl
C 288	8	42.1	19	3	US-09-814-252-10	Sequence 34, Appl	361	7.8	41.1	19	3	US-09-672-717-28	Sequence 28, Appl
C 289	8	42.1	19	3	US-09-814-252-10	Sequence 6, Appl	C 362	7.8	41.1	19	3	US-09-303-013-4	Sequence 4, Appl
C 290	8	42.1	19	4	US-09-310-844C-34	Sequence 19, Appl	363	7.8	41.1	19	3	US-09-533-149-5	Sequence 5, Appl
C 291	8	42.1	19	4	US-09-977-668-34	Sequence 19, Appl	C 364	7.8	41.1	19	3	US-09-634-960A-29	Sequence 29, Appl
292	8	42.1	19	5	US-10-032-495A-6	Sequence 6, Appl	C 365	7.8	41.1	19	3	US-09-696-791-2476	Sequence 2476, Ap
293	8	42.1	19	5	US-10-032-495A-14	Sequence 14, Appl	C 366	7.8	41.1	19	3	US-09-696-791-2477	Sequence 2477, Ap
294	8	42.1	19	5	US-10-032-495A-19	Sequence 19, Appl	367	7.8	41.1	19	3	US-09-696-791-2478	Sequence 2478, Ap
295	8	42.1	19	7	PCT-US94-13041-5	Sequence 5, Appl	368	7.8	41.1	19	3	US-09-696-791-2479	Sequence 2479, Ap
296	8	42.1	19	7	PCT-US95-02865-5	Sequence 5, Appl	369	7.8	41.1	19	3	US-09-696-791-401	Sequence 439, Ap
297	8	42.1	19	10	5217865-9	Patent No. 5217865	C 370	7.8	41.1	19	3	US-09-696-791-801	Sequence 801, Ap
298	8	42.1	19	10	5217865-9	Patent No. 5217865	C 371	7.8	41.1	19	3	US-09-696-791-802	Sequence 802, Ap
299	7.8	41.1	19	2	US-08-063-167A-43	Sequence 43, Appl	C 372	7.8	41.1	19	3	US-09-696-791-1854	Sequence 1854, Ap
300	7.8	41.1	19	2	US-08-315-695-13	Sequence 13, Appl	373	7.8	41.1	19	3	US-09-696-791-1855	Sequence 1855, Ap
301	7.8	41.1	19	2	US-08-007-997A-43	Sequence 36, Appl	374	7.8	41.1	19	3	US-09-696-791-1902	Sequence 1902, Ap
302	7.8	41.1	19	2	US-08-411-020-36	Sequence 56, Appl	C 375	7.8	41.1	19	3	US-09-696-791-2154	Sequence 2154, Ap
303	7.8	41.1	19	2	US-08-411-020-56	Sequence 56, Appl	C 376	7.8	41.1	19	3	US-09-696-791-2155	Sequence 2155, Ap
304	7.8	41.1	19	2	US-08-411-020-58	Sequence 58, Appl	C 377	7.8	41.1	19	3	US-09-696-791-2156	Sequence 2156, Ap
305	7.8	41.1	19	2	US-08-446-530-3	Sequence 3, Appl	C 378	7.8	41.1	19	3	US-09-696-791-2581	Sequence 2581, Ap
306	7.8	41.1	19	2	US-08-832-883-28	Sequence 28, Appl	C 379	7.8	41.1	19	3	US-09-696-791-2583	Sequence 2583, Ap
307	7.8	41.1	19	2	US-08-410-779B-58	Sequence 58, Appl	380	7.8	41.1	19	3	US-09-696-791-2584	Sequence 2584, Ap
308	7.8	41.1	19	2	US-08-410-779B-58	Sequence 60, Appl	381	7.8	41.1	19	3	US-09-696-791-3075	Sequence 3075, Ap
309	7.8	41.1	19	2	US-08-410-779B-84	Sequence 84, Appl	382	7.8	41.1	19	3	US-09-696-791-3143	Sequence 3143, Ap
310	7.8	41.1	19	2	US-08-410-779B-100	Sequence 100, Ap	C 383	7.8	41.1	19	3	US-09-696-791-2581	Sequence 2581, Ap
311	7.8	41.1	19	2	US-08-410-779B-122	Sequence 122, Ap	C 384	7.8	41.1	19	3	US-09-696-791-2582	Sequence 2582, Ap
312	7.8	41.1	19	2	US-08-410-779B-130	Sequence 130, Ap	C 385	7.8	41.1	19	3	US-09-696-791-2583	Sequence 2583, Ap
C 313	7.8	41.1	19	2	US-08-331-389A-10	Sequence 10, Appl	C 386	7.8	41.1	19	3	US-09-696-791-3075	Sequence 3075, Ap
C 314	7.8	41.1	19	2	US-08-331-389A-14	Sequence 14, Appl	C 387	7.8	41.1	19	3	US-09-696-791-3143	Sequence 3143, Ap
315	7.8	41.1	19	2	US-08-832-877-28	Sequence 28, Appl	C 388	7.8	41.1	19	3	US-09-696-791-3143	Sequence 3143, Ap

c 389	7.8	41.1	19	3	US-09-696-791-3326	Sequence 3326, Ap	462	7.6	40.0	19	3	US-09-696-791-403	Sequence 403, App
390	7.8	41.1	19	3	US-09-696-791-3744	Sequence 3744, Ap	c 463	7.6	40.0	19	3	US-09-696-791-774	Sequence 774, App
391	7.8	41.1	19	3	US-09-696-791-3745	Sequence 3745, Ap	c 464	7.6	40.0	19	3	US-09-696-791-775	Sequence 775, App
392	7.8	41.1	19	3	US-09-696-791-3746	Sequence 3746, Ap	c 465	7.6	40.0	19	3	US-09-696-791-1676	Sequence 1676, Ap
393	7.8	41.1	19	3	US-09-696-791-3747	Sequence 3747, Ap	c 466	7.6	40.0	19	3	US-09-696-791-1577	Sequence 1577, Ap
394	7.8	41.1	19	3	US-09-696-791-3748	Sequence 3748, Ap	c 467	7.6	40.0	19	3	US-09-696-791-1528	Sequence 1528, Ap
395	7.8	41.1	19	3	US-10-330-562-46	Sequence 46, Appl	c 468	7.6	40.0	19	3	US-09-696-791-2013	Sequence 2013, Ap
c 396	7.8	41.1	19	3	US-10-071-411A-17	Sequence 17, Appl	c 469	7.6	40.0	19	3	US-09-696-791-2588	Sequence 2588, Ap
397	7.8	41.1	19	3	US-09-627-1658-18	Sequence 18, Appl	c 470	7.6	40.0	19	3	US-09-696-791-3920	Sequence 3920, Ap
398	7.8	41.1	19	3	US-09-982-262C-43	Sequence 43, Appl	c 471	7.6	40.0	19	3	US-09-696-791-3968	Sequence 3968, Ap
399	7.8	41.1	19	3	US-09-647-501-24	Sequence 24, Appl	c 472	7.6	40.0	19	3	US-09-696-791-3869	Sequence 3869, Ap
c 400	7.8	41.1	19	3	US-09-882-434A-6	Sequence 6, Appl1	c 473	7.6	40.0	19	3	US-09-720-435A-9	Sequence 9, Appl1
c 401	7.8	41.1	19	3	US-10-199-945A-18	Sequence 18, Appl	c 474	7.6	40.0	19	3	US-09-719-737-14	Sequence 14, Appl1
c 402	7.8	41.1	19	3	US-09-830-902-70	Sequence 70, Appl	c 475	7.6	40.0	19	3	US-09-850-514-1	Sequence 1, Appl1
c 403	7.8	41.1	19	3	US-09-832-424-10	Sequence 10, Appl	c 476	7.6	40.0	19	3	US-09-502-498C-133	Sequence 133, App
c 404	7.8	41.1	19	3	US-09-970-532-6	Sequence 6, Appl1	c 477	7.6	40.0	19	3	US-09-502-498C-134	Sequence 134, App
c 405	7.8	41.1	19	3	US-09-935-338-183	Sequence 183, App	c 478	7.6	40.0	19	3	US-09-865-807-33	Sequence 33, Appl
c 406	7.8	41.1	19	3	US-09-935-338-200	Sequence 200, App	c 479	7.6	40.0	19	3	US-09-735-271-1440	Sequence 1440, Ap
c 407	7.8	41.1	19	4	US-09-855-309-15	Sequence 15, Appl	c 480	7.6	40.0	19	3	US-09-807-201-23	Sequence 23, Appl
c 408	7.8	41.1	19	5	US-09-543-679A-1394	Sequence 1394, Ap	c 481	7.6	40.0	19	3	US-09-502-424C-133	Sequence 133, App
c 409	7.8	41.1	19	7	PCT-US93-08101-43	Sequence 43, Appl	c 482	7.6	40.0	19	3	PCT-US95-05265-38	Sequence 38, Appl
c 410	7.8	41.1	19	7	PCT-US94-03437-18	Sequence 18, Appl	c 483	7.6	40.0	19	3	US-09-543-679A-1514	Sequence 1514, Ap
c 411	7.8	41.1	19	7	PCT-US95-04477-58	Sequence 58, Appl	c 484	7.6	40.0	19	4	US-10-270-861-29	Sequence 29, Appl
c 412	7.8	41.1	19	7	PCT-US95-04477-68	Sequence 68, Appl	c 485	7.6	40.0	19	4	US-09-977-868-33	Sequence 33, Appl
c 413	7.8	41.1	19	7	PCT-US95-04477-84	Sequence 84, Appl	c 486	7.6	40.0	19	5	US-09-543-679A-1514	Sequence 1514, Ap
c 414	7.8	41.1	19	7	PCT-US95-04477-100	Sequence 100, App	c 487	7.6	40.0	19	7	PCT-US95-05265-38	Sequence 38, Appl
c 415	7.8	41.1	19	7	PCT-US95-04477-122	Sequence 122, App	c 488	7.4	38.9	19	2	US-08-242-664-11	Sequence 11, Appl
c 416	7.8	41.1	19	7	PCT-US95-04477-130	Sequence 130, App	c 489	7.4	38.9	19	2	US-08-223-177A-78	Sequence 78, Appl
c 417	7.6	40.0	19	2	US-08-235-503B-138	Sequence 38, Appl	c 490	7.4	38.9	19	2	US-08-199-152-1	Sequence 1, Appl1
c 418	7.6	40.0	19	2	US-08-105-168B-12	Sequence 12, Appl	c 491	7.4	38.9	19	2	US-08-266-414-9	Sequence 9, Appl1
c 419	7.6	40.0	19	2	US-08-358-782D-3	Sequence 3, Appl1	c 492	7.4	38.9	19	2	US-08-631-200-47	Sequence 47, Appl
c 420	7.6	40.0	19	2	US-08-445-289B-14	Sequence 14, Appl	c 493	7.4	38.9	19	2	US-08-450-257-66	Sequence 66, Appl
c 421	7.6	40.0	19	2	US-08-564-860A-3	Sequence 3, Appl1	c 494	7.4	38.9	19	2	US-08-450-257-67	Sequence 67, Appl
c 422	7.6	40.0	19	2	US-08-698-948-12	Sequence 12, Appl	c 495	7.4	38.9	19	2	US-08-484-138-11	Sequence 11, Appl
c 423	7.6	40.0	19	2	US-08-117-952-98	Sequence 98, Appl	c 496	7.4	38.9	19	2	US-08-450-246-66	Sequence 66, Appl
c 424	7.6	40.0	19	2	US-08-764-527A-3	Sequence 3, Appl1	c 497	7.4	38.9	19	2	US-08-450-246-67	Sequence 67, Appl
c 425	7.6	40.0	19	2	US-08-910-367-7	Sequence 7, Appl1	c 498	7.4	38.9	19	2	US-08-450-098-66	Sequence 66, Appl
c 426	7.6	40.0	19	2	US-08-519-547A-2	Sequence 2, Appl1	c 499	7.4	38.9	19	2	US-08-450-098-67	Sequence 67, Appl
c 427	7.6	40.0	19	2	US-09-013-114-3	Sequence 3, Appl1	c 500	7.4	38.9	19	2	US-08-229-145-23	Sequence 23, Appl
c 428	7.6	40.0	19	3	US-09-133-934-10	Sequence 10, Appl	c 501	7.4	38.9	19	2	US-08-462-305-18	Sequence 18, Appl
c 429	7.6	40.0	19	3	US-09-014-416-54	Sequence 54, Appl	c 502	7.4	38.9	19	2	US-08-171-718-82	Sequence 82, Appl
c 430	7.6	40.0	19	3	US-09-050-159-27	Sequence 27, Appl	c 503	7.4	38.9	19	2	US-08-582-539-29	Sequence 29, Appl
c 431	7.6	40.0	19	3	US-09-288-586-7	Sequence 7, Appl1	c 504	7.4	38.9	19	2	US-08-451-233-66	Sequence 66, Appl
c 432	7.6	40.0	19	3	US-08-836-261A-40	Sequence 40, Appl	c 505	7.4	38.9	19	2	US-08-451-233-67	Sequence 67, Appl
c 433	7.6	40.0	19	3	US-09-290-577-33	Sequence 33, Appl	c 506	7.4	38.9	19	2	US-08-450-236-66	Sequence 66, Appl
c 434	7.6	40.0	19	3	US-09-338-907-535	Sequence 535, App	c 507	7.4	38.9	19	2	US-08-450-236-67	Sequence 67, Appl
c 435	7.6	40.0	19	3	US-09-297-535-22	Sequence 22, Appl	c 508	7.4	38.9	19	2	US-08-912-976-28	Sequence 28, Appl
c 436	7.6	40.0	19	3	US-09-290-452-33	Sequence 33, Appl	c 509	7.4	38.9	19	2	US-08-410-779B-76	Sequence 76, Appl
c 437	7.6	40.0	19	3	US-09-290-338-33	Sequence 33, Appl	c 510	7.4	38.9	19	2	US-08-829-553-47	Sequence 47, Appl
c 438	7.6	40.0	19	3	US-09-218-207-535	Sequence 535, App	c 511	7.4	38.9	19	2	US-08-829-553-47	Sequence 47, Appl
c 439	7.6	40.0	19	3	US-09-342-681C-81	Sequence 81, Appl	c 512	7.4	38.9	19	2	US-08-267-803B-71	Sequence 71, Appl
c 440	7.6	40.0	19	3	US-09-531-000-40	Sequence 40, Appl	c 513	7.4	38.9	19	2	US-08-331-389A-22	Sequence 22, Appl
c 441	7.6	40.0	19	3	US-09-291-129-6	Sequence 6, Appl1	c 514	7.4	38.9	19	2	US-08-633-501-12	Sequence 12, Appl
c 442	7.6	40.0	19	3	US-09-290-000-33	Sequence 33, Appl	c 515	7.4	38.9	19	2	US-08-633-501-106	Sequence 106, App
c 443	7.6	40.0	19	3	US-09-422-978-4222	Sequence 4222, Ap	c 516	7.4	38.9	19	2	US-08-757-653-118	Sequence 118, App
c 444	7.6	40.0	19	3	US-09-422-978-5276	Sequence 5276, Ap	c 517	7.4	38.9	19	2	US-08-607-384A-26	Sequence 26, Appl
c 445	7.6	40.0	19	3	US-09-422-978-6102	Sequence 6102, Ap	c 518	7.4	38.9	19	2	US-08-593-345B-4	Sequence 4, Appl1
c 446	7.6	40.0	19	3	US-09-422-978-6782	Sequence 6782, Ap	c 519	7.4	38.9	19	2	US-08-922-267A-47	Sequence 47, Appl1
c 447	7.6	40.0	19	3	US-09-422-978-7450	Sequence 7450, Ap	c 520	7.4	38.9	19	2	US-08-173-489C-28	Sequence 28, Appl
c 448	7.6	40.0	19	3	US-09-422-978-8701	Sequence 8701, Ap	c 521	7.4	38.9	19	2	US-08-882-083-12	Sequence 12, Appl
c 449	7.6	40.0	19	3	US-09-422-978-8719	Sequence 8719, Ap	c 522	7.4	38.9	19	2	US-08-936-707A-47	Sequence 47, Appl
c 450	7.6	40.0	19	3	US-09-422-978-9763	Sequence 9763, Ap	c 523	7.4	38.9	19	2	US-08-613-417A-18	Sequence 18, Appl
c 451	7.6	40.0	19	3	US-09-422-978-10748	Sequence 10748, A	c 524	7.4	38.9	19	2	US-08-936-706A-47	Sequence 47, Appl
c 452	7.6	40.0	19	3	US-09-422-978-11405	Sequence 11405, A	c 525	7.4	38.9	19	2	US-08-699-485-33	Sequence 33, Appl
c 453	7.6	40.0	19	3	US-09-954-594A-33	Sequence 33, Appl	c 526	7.4	38.9	19	2	US-08-532-777A-2	Sequence 2, Appl1
c 454	7.6	40.0	19	3	US-09-982-212-33	Sequence 33, Appl	c 527	7.4	38.9	19	2	US-08-587-332B-4	Sequence 4, Appl1
c 455	7.6	40.0	19	3	US-09-261-104-11	Sequence 11, Appl	c 528	7.4	38.9	19	2	US-08-558-107-12	Sequence 12, Appl
c 456	7.6	40.0	19	3	US-09-747-391-105	Sequence 105, App	c 529	7.4	38.9	19	2	US-08-690-494-33	Sequence 33, Appl
c 457	7.6	40.0	19	3	US-09-672-717-46	Sequence 46, Appl	c 530	7.4	38.9	19	2	US-08-475-634D-12	Sequence 12, Appl
c 458	7.6	40.0	19	3	US-09-672-717-120	Sequence 120, App	c 531	7.4	38.9	19	2	US-08-756-386-54	Sequence 54, Appl
c 459	7.6	40.0	19	3	US-08-401-192-4	Sequence 4, Appl1	c 532	7.4	38.9	19	2	US-08-743-637B-67	Sequence 67, Appl
c 460	7.6	40.0	19	3	US-09-763-590-23	Sequence 23, Appl	c 533	7.4	38.9	19	2	US-08-823-516-43	Sequence 43, Appl
c 461	7.6	40.0	19	3	US-09-696-791-219	Sequence 219, App	c 534	7.4	38.9	19	3	US-08-526-840B-67	Sequence 67, Appl

535	7.4	38.9	19	3	US-08-682-853A-54	Sequence 54, App1	608	7.4	38.9	19	3	US-09-422-978-4894	Sequence 4894, Ap
C 536	7.4	38.9	19	3	US-08-594-452-18	Sequence 18, App1	C 609	7.4	38.9	19	3	US-09-422-978-4919	Sequence 4919, Ap
C 537	7.4	38.9	19	3	US-08-578-686C-17	Sequence 17, App1	C 610	7.4	38.9	19	3	US-09-422-978-5133	Sequence 5133, Ap
538	7.4	38.9	19	3	US-03-044-946-12	Sequence 12, App1	C 611	7.4	38.9	19	3	US-09-422-978-5350	Sequence 5350, Ap
C 539	7.4	38.9	19	3	US-03-044-946-106	Sequence 106, App1	C 612	7.4	38.9	19	3	US-09-422-978-5491	Sequence 5491, Ap
C 540	7.4	38.9	19	3	US-08-281-203-13	Sequence 13, App1	C 613	7.4	38.9	19	3	US-09-422-978-5595	Sequence 5595, Ap
C 541	7.4	38.9	19	3	US-03-248-203-47	Sequence 47, App1	C 614	7.4	38.9	19	3	US-09-422-978-6132	Sequence 6132, Ap
C 542	7.4	38.9	19	3	US-08-485-942A-39	Sequence 39, App1	C 615	7.4	38.9	19	3	US-09-422-978-6518	Sequence 6518, Ap
C 543	7.4	38.9	19	3	US-03-094-405-20	Sequence 20, App1	C 616	7.4	38.9	19	3	US-09-422-978-6991	Sequence 6991, Ap
544	7.4	38.9	19	3	US-08-478-087-82	Sequence 82, App1	C 617	7.4	38.9	19	3	US-09-422-978-7108	Sequence 7108, Ap
545	7.4	38.9	19	3	US-08-777-266A-98	Sequence 98, App1	C 618	7.4	38.9	19	3	US-09-422-978-7342	Sequence 7342, Ap
C 546	7.4	38.9	19	3	US-08-660-645A-47	Sequence 47, App1	C 619	7.4	38.9	19	3	US-09-422-978-7368	Sequence 7368, Ap
547	7.4	38.9	19	3	US-08-759-038-54	Sequence 54, App1	C 620	7.4	38.9	19	3	US-09-422-978-7851	Sequence 7851, Ap
548	7.4	38.9	19	3	US-08-855-372B-84	Sequence 84, App1	C 621	7.4	38.9	19	3	US-09-422-978-8354	Sequence 8354, Ap
549	7.4	38.9	19	3	US-08-758-314-54	Sequence 54, App1	C 622	7.4	38.9	19	3	US-09-422-978-9226	Sequence 9226, Ap
550	7.4	38.9	19	3	US-03-058-489-62	Sequence 62, App1	C 623	7.4	38.9	19	3	US-09-422-978-10828	Sequence 10828, A
C 551	7.4	38.9	19	3	US-03-258-408-18	Sequence 18, App1	C 624	7.4	38.9	19	3	US-09-422-978-825A-54	Sequence 54, App1
552	7.4	38.9	19	3	US-09-044-908-12	Sequence 12, App1	C 625	7.4	38.9	19	3	US-09-399-217-33	Sequence 33, App1
553	7.4	38.9	19	3	US-09-044-908-106	Sequence 106, App1	C 626	7.4	38.9	19	3	US-09-356-806-49	Sequence 49, App1
C 554	7.4	38.9	19	3	US-09-048-214A-39	Sequence 39, App1	C 627	7.4	38.9	19	3	US-09-356-806-71	Sequence 71, App1
C 555	7.4	38.9	19	3	US-08-488-208A-39	Sequence 39, App1	C 628	7.4	38.9	19	3	US-09-356-806-71	Sequence 71, App1
C 556	7.4	38.9	19	3	US-03-136-132-18	Sequence 18, App1	C 629	7.4	38.9	19	3	US-09-814-986-47	Sequence 47, App1
C 557	7.4	38.9	19	3	US-03-243-539-12	Sequence 12, App1	C 630	7.4	38.9	19	3	US-08-465-679-24	Sequence 24, App1
C 558	7.4	38.9	19	3	US-09-144-112-17	Sequence 17, App1	C 631	7.4	38.9	19	3	US-09-547-267-47	Sequence 47, App1
C 559	7.4	38.9	19	3	US-09-192-657A-22	Sequence 22, App1	C 632	7.4	38.9	19	3	US-09-582-212-32	Sequence 32, App1
C 560	7.4	38.9	19	3	US-03-378-528-4	Sequence 4, App1	C 633	7.4	38.9	19	3	US-08-210-143C-22	Sequence 22, App1
561	7.4	38.9	19	3	US-03-406-071-47	Sequence 47, App1	C 634	7.4	38.9	19	3	US-09-456-222B-2	Sequence 2, App1
C 562	7.4	38.9	19	3	US-08-962-690-47	Sequence 47, App1	C 635	7.4	38.9	19	3	US-09-495-791-111	Sequence 111, App1
C 563	7.4	38.9	19	3	US-08-962-690-37	Sequence 37, App1	C 636	7.4	38.9	19	3	US-09-495-791-111	Sequence 111, App1
C 564	7.4	38.9	19	3	US-09-262-773-22	Sequence 22, App1	C 637	7.4	38.9	19	3	US-09-495-791-111	Sequence 111, App1
565	7.4	38.9	19	3	US-03-385-377-9	Sequence 9, App1	C 638	7.4	38.9	19	3	US-09-655-778A-118	Sequence 118, App1
C 566	7.4	38.9	19	3	US-03-038-637-82	Sequence 82, App1	C 639	7.4	38.9	19	3	US-09-672-717-43	Sequence 43, App1
C 567	7.4	38.9	19	3	US-09-034-867-147	Sequence 147, App1	C 640	7.4	38.9	19	3	US-09-672-717-132	Sequence 132, App1
C 568	7.4	38.9	19	3	US-09-052-333A-50	Sequence 50, App1	C 641	7.4	38.9	19	3	US-09-672-717-172	Sequence 172, App1
570	7.4	38.9	19	3	US-09-338-907-419	Sequence 419, App1	C 642	7.4	38.9	19	3	US-09-672-717-181	Sequence 181, App1
C 571	7.4	38.9	19	3	US-09-338-907-431	Sequence 431, App1	C 643	7.4	38.9	19	3	US-09-920-923B-26	Sequence 26, App1
C 572	7.4	38.9	19	3	US-09-338-907-569	Sequence 569, App1	C 644	7.4	38.9	19	3	US-09-940-244-43	Sequence 43, App1
574	7.4	38.9	19	3	US-08-803-946-51	Sequence 51, App1	C 645	7.4	38.9	19	3	US-09-333-145-54	Sequence 54, App1
C 575	7.4	38.9	19	3	US-08-960-632-26	Sequence 26, App1	C 646	7.4	38.9	19	3	US-08-983-605-120	Sequence 120, App1
C 576	7.4	38.9	19	3	US-09-439-616-3	Sequence 3, App1	C 647	7.4	38.9	19	3	US-08-983-605-220	Sequence 220, App1
C 577	7.4	38.9	19	3	US-08-483-211A-39	Sequence 39, App1	C 648	7.4	38.9	19	3	US-09-696-791-35	Sequence 35, App1
C 578	7.4	38.9	19	3	US-08-235-403-67	Sequence 67, App1	C 649	7.4	38.9	19	3	US-09-696-791-55	Sequence 55, App1
579	7.4	38.9	19	3	US-08-895-981-18	Sequence 18, App1	C 650	7.4	38.9	19	3	US-09-696-791-266	Sequence 266, App1
C 580	7.4	38.9	19	3	US-09-564-805-105	Sequence 105, App1	C 651	7.4	38.9	19	3	US-09-696-791-267	Sequence 267, App1
582	7.4	38.9	19	3	US-09-218-207-419	Sequence 419, App1	C 652	7.4	38.9	19	3	US-09-696-791-308	Sequence 308, App1
C 583	7.4	38.9	19	3	US-09-218-207-431	Sequence 431, App1	C 653	7.4	38.9	19	3	US-09-696-791-438	Sequence 438, App1
C 584	7.4	38.9	19	3	US-08-337-120A-20	Sequence 20, App1	C 654	7.4	38.9	19	3	US-09-696-791-546	Sequence 546, App1
C 585	7.4	38.9	19	3	US-09-350-309-54	Sequence 54, App1	C 655	7.4	38.9	19	3	US-09-696-791-705	Sequence 705, App1
586	7.4	38.9	19	3	US-08-488-223A-39	Sequence 39, App1	C 656	7.4	38.9	19	3	US-09-696-791-707	Sequence 707, App1
C 587	7.4	38.9	19	3	US-08-520-946-118	Sequence 118, App1	C 657	7.4	38.9	19	3	US-09-696-791-1288	Sequence 1288, App1
C 588	7.4	38.9	19	3	US-08-294-312B-24	Sequence 24, App1	C 658	7.4	38.9	19	3	US-09-696-791-1289	Sequence 1289, App1
C 589	7.4	38.9	19	3	US-08-458-831A-39	Sequence 39, App1	C 659	7.4	38.9	19	3	US-09-696-791-1338	Sequence 1338, App1
C 590	7.4	38.9	19	3	US-08-458-831A-39	Sequence 39, App1	C 660	7.4	38.9	19	3	US-09-696-791-1671	Sequence 1671, App1
C 591	7.4	38.9	19	3	US-09-531-000-7	Sequence 7, App1	C 661	7.4	38.9	19	3	US-09-696-791-1672	Sequence 1672, App1
592	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 662	7.4	38.9	19	3	US-09-696-791-1673	Sequence 1673, App1
C 593	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 663	7.4	38.9	19	3	US-09-696-791-1674	Sequence 1674, App1
C 594	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 664	7.4	38.9	19	3	US-09-696-791-1674	Sequence 1674, App1
C 595	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 665	7.4	38.9	19	3	US-09-696-791-1943	Sequence 1943, App1
C 596	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 666	7.4	38.9	19	3	US-09-696-791-2217	Sequence 2217, App1
C 597	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 667	7.4	38.9	19	3	US-09-696-791-2216	Sequence 2216, App1
C 598	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 668	7.4	38.9	19	3	US-09-696-791-2217	Sequence 2217, App1
C 599	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 669	7.4	38.9	19	3	US-09-696-791-2218	Sequence 2218, App1
C 600	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 670	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, App1
C 601	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 671	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, App1
C 602	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 672	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, App1
C 603	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 673	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, App1
C 604	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 674	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, App1
C 605	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 675	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, App1
C 606	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 676	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, App1
C 607	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 677	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, App1
							C 678	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, App1
							C 679	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, App1
							C 680	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, App1

681	7.4	38.9	19	3	US-09-696-791-3414	Sequence 3414, Ap	c 754	7.2	37.9	19	2	US-08-549-045-12	Sequence 12, Appl
682	7.4	38.9	19	3	US-09-696-791-3415	Sequence 3415, Ap	c 755	7.2	37.9	19	2	US-08-650-125-8	Sequence 8, Appl
683	7.4	38.9	19	3	US-09-696-791-3416	Sequence 3416, Ap	c 756	7.2	37.9	19	2	US-08-795-006A-8	Sequence 8, Appl
684	7.4	38.9	19	3	US-09-696-791-3417	Sequence 3417, Ap	c 757	7.2	37.9	19	2	US-08-270-581-5	Sequence 5, Appl
685	7.4	38.9	19	3	US-09-696-791-3418	Sequence 3418, Ap	c 758	7.2	37.9	19	2	US-08-485-689-4	Sequence 44, Appl
c 686	7.4	38.9	19	3	US-09-696-791-3419	Sequence 3419, Ap	c 759	7.2	37.9	19	2	US-08-450-905B-155	Sequence 155, App
687	7.4	38.9	19	3	US-09-696-791-3488	Sequence 3488, Ap	c 760	7.2	37.9	19	2	US-08-716-718-7	Sequence 44, Appl
688	7.4	38.9	19	3	US-09-696-791-3489	Sequence 3489, Ap	c 761	7.2	37.9	19	2	US-08-476-021A-4	Sequence 7, Appl
689	7.4	38.9	19	3	US-09-696-791-3490	Sequence 3490, Ap	c 762	7.2	37.9	19	2	US-08-743-200-25	Sequence 25, Appl
690	7.4	38.9	19	3	US-09-696-791-3491	Sequence 3491, Ap	c 763	7.2	37.9	19	2	US-08-914-512-12	Sequence 12, Appl
691	7.4	38.9	19	3	US-09-696-791-3509	Sequence 3509, Ap	c 764	7.2	37.9	19	2	US-08-478-608B-44	Sequence 44, Appl
692	7.4	38.9	19	3	US-09-696-791-3510	Sequence 3510, Ap	c 765	7.2	37.9	19	2	US-08-282-197C-19	Sequence 19, Appl
693	7.4	38.9	19	3	US-09-696-791-3511	Sequence 3511, Ap	c 766	7.2	37.9	19	2	US-08-690-495-36	Sequence 36, Appl
694	7.4	38.9	19	3	US-09-696-791-3512	Sequence 3512, Ap	c 767	7.2	37.9	19	2	US-08-912-129A-53	Sequence 63, Appl
c 695	7.4	38.9	19	3	US-09-696-791-3583	Sequence 3583, Ap	c 768	7.2	37.9	19	2	US-08-912-129A-83	Sequence 83, Appl
696	7.4	38.9	19	3	US-09-696-791-3743	Sequence 3743, Ap	c 769	7.2	37.9	19	2	US-08-690-494-36	Sequence 36, Appl
697	7.4	38.9	19	3	US-09-696-791-3876	Sequence 3876, Ap	c 770	7.2	37.9	19	2	US-08-849-021-75	Sequence 75, Appl
698	7.4	38.9	19	3	US-09-696-791-3877	Sequence 3877, Ap	c 771	7.2	37.9	19	2	US-09-212-771-3	Sequence 3, Appl
699	7.4	38.9	19	3	US-09-696-791-3878	Sequence 3878, Ap	c 772	7.2	37.9	19	2	US-08-690-184-2	Sequence 2, Appl
700	7.4	38.9	19	3	US-09-696-791-3879	Sequence 3879, Ap	c 773	7.2	37.9	19	3	US-08-485-942A-81	Sequence 81, Appl
c 701	7.4	38.9	19	3	US-09-696-791-3921	Sequence 3921, Ap	c 774	7.2	37.9	19	3	US-07-982-759F-155	Sequence 155, App
c 702	7.4	38.9	19	3	US-09-835-370-19	Sequence 19, Appl	c 775	7.2	37.9	19	3	US-08-881-784-28	Sequence 28, Appl
703	7.4	38.9	19	3	US-09-404-448-3	Sequence 3, Appl	c 776	7.2	37.9	19	3	US-08-787-091-10	Sequence 10, Appl
704	7.4	38.9	19	3	US-10-320-176-10	Sequence 10, Appl	c 777	7.2	37.9	19	3	US-08-488-21A-81	Sequence 81, Appl
705	7.4	38.9	19	3	US-10-320-176-12	Sequence 12, Appl	c 778	7.2	37.9	19	3	US-08-488-208A-81	Sequence 81, Appl
706	7.4	38.9	19	3	US-09-490-700-18	Sequence 18, Appl	c 779	7.2	37.9	19	3	US-09-291-823-2	Sequence 2, Appl
707	7.4	38.9	19	3	US-09-434-382-105	Sequence 105, App	c 780	7.2	37.9	19	3	US-08-938-669A-11	Sequence 11, Appl
708	7.4	38.9	19	3	US-10-309-438-33	Sequence 33, Appl	c 781	7.2	37.9	19	3	US-08-161-674B-17	Sequence 17, Appl
709	7.4	38.9	19	3	US-09-381-212-43	Sequence 43, Appl	c 782	7.2	37.9	19	3	US-09-184-073-8	Sequence 8, Appl
710	7.4	38.9	19	3	US-10-081-806-54	Sequence 54, Appl	c 783	7.2	37.9	19	3	US-09-292-768-29	Sequence 29, Appl
c 711	7.4	38.9	19	3	US-09-928-796-3	Sequence 3, Appl	c 784	7.2	37.9	19	3	US-09-050-159-56	Sequence 56, Appl
c 712	7.4	38.9	19	3	US-09-623-828C-15	Sequence 15, Appl	c 785	7.2	37.9	19	3	US-08-856-963-6	Sequence 6, Appl
713	7.4	38.9	19	3	US-09-646-533D-34	Sequence 34, Appl	c 786	7.2	37.9	19	3	US-08-856-963-10	Sequence 10, Appl
c 714	7.4	38.9	19	3	US-09-835-371-19	Sequence 19, Appl	c 787	7.2	37.9	19	3	US-08-856-963-18	Sequence 18, Appl
715	7.4	38.9	19	3	US-09-713-601A-43	Sequence 43, Appl	c 788	7.2	37.9	19	3	US-08-856-963-22	Sequence 22, Appl
c 716	7.4	38.9	19	3	US-09-793-146-17	Sequence 17, Appl	c 789	7.2	37.9	19	3	US-08-476-423A-44	Sequence 44, Appl
717	7.4	38.9	19	3	US-09-693-333-169	Sequence 169, App	c 790	7.2	37.9	19	3	US-08-833-624-20	Sequence 20, Appl
c 718	7.4	38.9	19	4	US-10-98-816-2	Sequence 2, Appl	c 791	7.2	37.9	19	3	US-09-338-907-476	Sequence 476, App
c 719	7.4	38.9	19	4	US-09-310-844C-32	Sequence 32, Appl	c 792	7.2	37.9	19	3	US-08-483-211A-81	Sequence 81, Appl
c 720	7.4	38.9	19	4	US-09-977-868-32	Sequence 32, Appl	c 793	7.2	37.9	19	3	US-09-457-208A-91	Sequence 9, Appl
c 721	7.4	38.9	19	4	US-10-114-908-28	Sequence 28, Appl	c 794	7.2	37.9	19	3	US-09-218-207-476	Sequence 476, App
c 722	7.4	38.9	19	4	US-10-114-908-213	Sequence 213, App	c 795	7.2	37.9	19	3	US-09-319-648-4	Sequence 4, Appl
723	7.4	38.9	19	4	US-10-114-908-214	Sequence 214, App	c 796	7.2	37.9	19	3	US-09-319-648-11	Sequence 11, Appl
c 724	7.4	38.9	19	4	US-10-222-825-17	Sequence 17, Appl	c 797	7.2	37.9	19	3	US-09-438-836A-7	Sequence 7, Appl
c 725	7.4	38.9	19	5	US-10-125-001-7	Sequence 7, Appl	c 798	7.2	37.9	19	3	US-09-319-648-41	Sequence 41, Appl
726	7.4	38.9	19	5	US-09-982-667-54	Sequence 54, Appl	c 799	7.2	37.9	19	3	US-08-430-812-20	Sequence 81, Appl
c 727	7.4	38.9	19	5	US-09-818-943-6	Sequence 6, Appl	c 800	7.2	37.9	19	3	US-09-144-367-44	Sequence 44, Appl
c 728	7.4	38.9	19	7	PCT-US91-03680-9	Sequence 9, Appl	c 801	7.2	37.9	19	3	US-09-470-443-87	Sequence 87, Appl
729	7.4	38.9	19	7	PCT-US95-04477-76	Sequence 76, Appl	c 802	7.2	37.9	19	3	US-09-319-648-4	Sequence 4, Appl
730	7.4	38.9	19	7	PCT-US95-04477-92	Sequence 92, Appl	c 803	7.2	37.9	19	3	US-09-319-648-11	Sequence 11, Appl
731	7.4	38.9	19	7	PCT-US95-06379-11	Sequence 11, Appl	c 804	7.2	37.9	19	3	US-09-150-661-4	Sequence 4, Appl
732	7.4	38.9	19	9	US-09-798-641-33	Sequence 33, Appl	c 805	7.2	37.9	19	3	US-09-146-893-5	Sequence 5, Appl
733	7.4	38.9	19	10	5262866-12	Sequence 10, Appl	c 806	7.2	37.9	19	3	US-08-488-225A-81	Sequence 81, Appl
c 734	7.2	37.9	19	2	US-07-689-008-10	Sequence 10, Appl	c 807	7.2	37.9	19	3	US-09-306-828-11	Sequence 11, Appl
c 735	7.2	37.9	19	2	US-07-661-378A-3	Sequence 3, Appl	c 808	7.2	37.9	19	3	US-09-216-393B-778	Sequence 278, App
c 736	7.2	37.9	19	2	US-08-093-884-1	Sequence 1, Appl	c 809	7.2	37.9	19	3	US-09-578-634A-1	Sequence 1, Appl
737	7.2	37.9	19	2	US-08-093-884-2	Sequence 2, Appl	c 810	7.2	37.9	19	3	US-09-661-596A-42	Sequence 42, Appl
c 738	7.2	37.9	19	2	US-08-093-884-3	Sequence 3, Appl	c 811	7.2	37.9	19	3	US-09-422-978-4453	Sequence 4453, Ap
739	7.2	37.9	19	2	US-07-918-318-22	Sequence 22, Appl	c 812	7.2	37.9	19	3	US-09-422-978-4539	Sequence 4539, Ap
c 740	7.2	37.9	19	2	US-08-379-296-10	Sequence 10, Appl	c 813	7.2	37.9	19	3	US-09-422-978-4653	Sequence 4653, Ap
c 741	7.2	37.9	19	2	US-08-779-295-10	Sequence 10, Appl	c 814	7.2	37.9	19	3	US-09-422-978-4917	Sequence 4917, Ap
c 742	7.2	37.9	19	2	US-08-779-296-7	Sequence 7, Appl	c 815	7.2	37.9	19	3	US-09-422-978-4951	Sequence 4951, Ap
c 743	7.2	37.9	19	2	US-08-779-296-10	Sequence 10, Appl	c 816	7.2	37.9	19	3	US-09-422-978-5022	Sequence 5022, Ap
744	7.2	37.9	19	2	US-08-379-081B-136	Sequence 136, App	c 817	7.2	37.9	19	3	US-09-422-978-5543	Sequence 5543, Ap
745	7.2	37.9	19	2	US-08-379-081B-137	Sequence 137, App	c 818	7.2	37.9	19	3	US-09-422-978-6003	Sequence 6003, Ap
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c 994      7 36.8      19 2 US-08-955-138-24      Sequence 24, Appl
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ALIGNMENTS

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; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens
US-09-672-717-29

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; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel

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; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSSET 020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; NUMBER OF SEQ ID NOS: 11796
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; ORGANISM: Homo Sapiens
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US-09-422-978-7559

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; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Trletz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
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; OTHER INFORMATION: Cyclin A1 ribozyme binding site
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; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Trletz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407

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CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-696-791-3128

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GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
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US-09-696-791-3129

Query Match 56.8%; Score 10.8; DB 3; Length 19;
Best Local Similarity 85.7%; Pred. No. 3.2e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Patent No. 6770633
GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3130
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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US-09-696-791-3130

Query Match 56.8%; Score 10.8; DB 3; Length 19;
Best Local Similarity 85.7%; Pred. No. 3.2e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCA 18
Db 4 CAGTTTCTCCTTCA 17

RESULT 7
US-09-696-791-3131
Sequence 3131, Application US/09696791
Patent No. 6770633
GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3131
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Cyclin A1 ribozyme binding site
US-09-696-791-3131

Query Match 56.8%; Score 10.8; DB 3; Length 19;
Best Local Similarity 85.7%; Pred. No. 3.2e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCA 18
Db 2 CAGTTTCTCCTTCA 15

RESULT 8
US-09-422-978-9324/C
Sequence 9324, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marca
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1998-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 9324
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..19
OTHER INFORMATION: downstream amplification primer 99-25005 for SEQ 1459, in compleme
US-09-422-978-9324

Query Match 55.8%; Score 10.6; DB 3; Length 19;
Best Local Similarity 76.5%; Pred. No. 4e+04;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CACGATCTCTTTCAC 19
||| ||| ||| ||| |||
Db 19 CACAGTCTCTTTTCAC 3

RESULT 9

US-09-422-978-4940
; Sequence 4940, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marla
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; EARLIER FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4940
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-18826 for SEQ 1006,
US-09-422-978-4940

Query Match 54.7%; Score 10.4; DB 3; Length 19;
Best Local Similarity 91.7%; Pred. No. 5.1e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTATCTCTTCA 18
||| ||| ||| ||| |||
Db 2 GTATCTCTTCA 13

RESULT 10

US-09-422-978-6219
; Sequence 6219, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marla
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; EARLIER FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6219
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-10173 for SEQ 2285,
US-09-422-978-6219

Query Match 54.7%; Score 10.4; DB 3; Length 19;
Best Local Similarity 91.7%; Pred. No. 5.1e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TATCTCTTTCAC 19
||| ||| ||| ||| |||
Db 4 TATCTCTTTCAC 15

RESULT 11

US-09-938-077-18/c
; Sequence 18, Application US/09938077
; Patent No. 6730500
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; TITLE OF INVENTION: Methods for Generating a Continuous
; FILE REFERENCE: Nucleotide Sequence from No. 6730500contiguous Nucleotide Sequen
; CURRENT APPLICATION NUMBER: US/09/938,077
; EARLIER FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Illustrative nucleotide sequence.
US-09-938-077-18

Query Match 54.7%; Score 10.4; DB 3; Length 19;
Best Local Similarity 91.7%; Pred. No. 5.1e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACGTATCTCTT 15
||| ||| ||| ||| |||
Db 18 AAGGTATCTCTT 7

RESULT 12

US-09-696-791-3132
; Sequence 3132, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Titz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; EARLIER FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3132
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cyclin A1 ribozyme binding site
US-09-696-791-3132

Query Match 54.7%; Score 10.4; DB 3; Length 19;
Best Local Similarity 91.7%; Pred. No. 5.1e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTATCTCTTCA 18
||| ||| ||| ||| |||
Db 1 GTTCTCTTCA 12

RESULT 13

US-08-182-619-2

Sequence 2, Application US/08182619
Patent No. 5484710
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Miyashita, Toshiyuki
APPLICANT: Harigai, Masayoshi
APPLICANT: Hanada, Motoi
TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING
TITLE OF INVENTION: AGENTS THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN
NUMBER OF INVENTION: 13
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,619
FILING DATE: 14-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9867
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-182-619-2

Query Match 52.6%; Score 10; DB 2; Length 19;
Best Local Similarity 72.2%; Pred. No. 8.2e+04;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GCACGATATCTCTTCAC 19
Db 2 GCACCTGAGCGCCTTCAC 19

RESULT 14
US-08-330-535A-2
Sequence 2, Application US/08330535A
Patent No. 5659024
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Miyashita, Toshiyuki
APPLICANT: Harigai, Masayoshi
APPLICANT: Hanada, Motoi
TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS
TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL
NUMBER OF INVENTION: DEATH
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,535A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,619
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-330-535A-2

Query Match 52.6%; Score 10; DB 2; Length 19;
Best Local Similarity 72.2%; Pred. No. 8.2e+04;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GCACGATATCTCTTCAC 19
Db 2 GCACCTGAGCGCCTTCAC 19

RESULT 15
US-08-838-844-2
Sequence 2, Application US/08838844
Patent No. 5908750
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Miyashita, Toshiyuki
APPLICANT: Harigai, Masayoshi
APPLICANT: Hanada, Motoi
TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS
TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL
NUMBER OF INVENTION: DEATH
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,844
FILING DATE: 11-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,619
FILING DATE: 14-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,535
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2520
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-838-844-2

Query Match 52.6%; Score 10; DB 2; Length 19;
Best Local Similarity 72.2%; Pred. No. 8.2e+04;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GCACGGTATCTCCTTAC 19
Db 2 GCACCTGAGCGCCTTAC 19

RESULT 16
US-08-851-350-26
Sequence 26, Application US/08851350
Patent No. 6057122
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
TITLE OF INVENTION: NOVEL ANTITUMORIC PEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,350
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TEXT:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-851-350-26

Query Match 52.6%; Score 10; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TATCTCCTTC 17

Db 8 TATCTCCTTC 17

RESULT 17
US-08-924-287A-26
Sequence 26, Application US/08924287A
Patent No. 669838
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
TITLE OF INVENTION: NOVEL ANTITUMORIC PEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS FOR INHIBITING
FILE REFERENCE: 5940.US.P3
CURRENT APPLICATION NUMBER: US/08/924,287A
CURRENT FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 08/851,350
PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: US 08/832,087
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: US 08/643,219
PRIOR FILING DATE: 1996-05-03
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PET3p-ATG Primer
US-08-924-287A-26

Query Match 52.6%; Score 10; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TATCTCCTTC 17
Db 8 TATCTCCTTC 17

RESULT 18
US-08-117-952-739
Sequence 739, Application US/08117952
Patent No. 5851760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretey, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Relfer, Stephen E.

REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 739:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Oligonucleotide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-117-952-739

Query Match 51.6%; Score 9.8; DB 2; Length 19;
Best Local Similarity 84.6%; Pred. No. 1e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGTATCTCCTTC 17
Db 3 CCGATCTCTCC 15

RESULT 19
US-08-549-004A-3/c
Sequence 3, Application US/08549004A
Patent No. 5869101
GENERAL INFORMATION:
APPLICANT: PENDERGAST, ANN MARIE
APPLICANT: DAI, ZONGHAN
TITLE OF INVENTION: ABL-INTERACTOR PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,004A
FILING DATE: 27-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-549-004A-3

Query Match 51.6%; Score 9.8; DB 2; Length 19;
Best Local Similarity 84.6%; Pred. No. 1e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GGTATCTCCTTC 18
Db 13 GGTATCTTCATCA 1

RESULT 20
US-09-051-982A-3/c
Sequence 3, Application US/09051982A
Patent No. 6255074
GENERAL INFORMATION:
APPLICANT: PENDERGAST, ANN MARIE
APPLICANT: DAI, ZONGHAN
TITLE OF INVENTION: ABL-INTERACTOR PROTEIN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,982A
FILING DATE: 08-JUL-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-051-982A-3

Query Match 51.6%; Score 9.8; DB 3; Length 19;
Best Local Similarity 84.6%; Pred. No. 1e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGTATCTCCTTC 18
Db 13 GGTATCTTCATCA 1

RESULT 21
US-08-815-795-2/c
Sequence 2, Application US/08815795
Patent No. 6271205
GENERAL INFORMATION:
APPLICANT: ROSE, ALONZO H.
APPLICANT: RECHT, LAWRENCE D.
APPLICANT: LACHYANKAR, MAHESH B.
TITLE OF INVENTION: CANCER TREATMENT BY EXPRESSION OF
TITLE OF INVENTION: DIFFERENTIATION FACTOR RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAPPIN & KUAMER
STREET: 200 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/815,795
FILING DATE:
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 06/310,287
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: WOZU-010C1P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-815-795-2
```

```
Query Match          51.6%; Score 9.8; DB 3; Length 19;
Best Local Similarity 84.6%; Pred. No. 1e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      7 GTATCTCCTTCAC 19
        |||||
DB      19 GTCTCTCTTCTC 7
```

```
RESULT 22
US-09-422-978-5993
; Sequence 5993, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marla
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; PRIORITY FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/299,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5993
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-8289 for SEQ 2059,
US-09-422-978-5993
```

```
Query Match          51.6%; Score 9.8; DB 3; Length 19;
Best Local Similarity 84.6%; Pred. No. 1e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      6 GGATCTCCTTCA 18
        |||||
DB      2 GGATTACTTCA 14
```

```
RESULT 23
US-10-130-158A-9
; Sequence 9, Application US/10130158A
; Patent No. 6844179
; GENERAL INFORMATION:
; APPLICANT: NAKANISHI, Atsushi
; APPLICANT: MORITA, Shigeru
; TITLE OF INVENTION: No. 6844179el protein and its DNA
; FILE REFERENCE: 2670USOP
; CURRENT APPLICATION NUMBER: US/10/130,158A
; PRIORITY FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: PCT/JP00/0805
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: JP 11-324467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 9
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-130-158A-9
```

```
Query Match          51.6%; Score 9.8; DB 3; Length 19;
Best Local Similarity 84.6%; Pred. No. 1e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      7 GTATCTCCTTCAC 19
        |||||
DB      5 GCATTTCTTCTAC 17
```

```
RESULT 24
US-10-130-158A-10/c
; Sequence 10, Application US/10130158A
; Patent No. 6844179
; GENERAL INFORMATION:
; APPLICANT: NAKANISHI, Atsushi
; APPLICANT: MORITA, Shigeru
; TITLE OF INVENTION: No. 6844179el protein and its DNA
; FILE REFERENCE: 2670USOP
; CURRENT APPLICATION NUMBER: US/10/130,158A
; PRIORITY FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: PCT/JP00/0805
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: JP 11-324467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 10
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-130-158A-10
```

```
Query Match          51.6%; Score 9.8; DB 3; Length 19;
Best Local Similarity 84.6%; Pred. No. 1e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 CACGGTATCTCCT 15
        |||||
DB      17 CACGGACCTCTCT 5
```

```
RESULT 25
US-09-108-006C-28/c
; Sequence 28, Application US/09108006C
; Patent No. 6524613
; GENERAL INFORMATION:
; APPLICANT: Steer, Clifford J.
```

Kren, Betsy T.
Bandyopadhyay, Paramita
Roy-Chowdhury, Jayanta
TITLE OF INVENTION: Hepatocellular Chimeraplasty
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kimeragen, Inc.
STREET: 300 Pheasant Run
CITY: Newtown
STATE: PA
COUNTRY: USA
ZIP: 18940
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,006C
FILING DATE: 30-Jun-1992
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,288
FILING DATE: 30-APR-1997
APPLICATION NUMBER: 60/054,837
FILING DATE: 05-AUG-1997
APPLICATION NUMBER: 60/064,996
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/074,497
FILING DATE: 12-FEB-1998
APPLICATION NUMBER: PCT US 98/08834
FILING DATE: 30-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Friedel, Thomas
REGISTRATION NUMBER: 29258
REFERENCE/DOCKET NUMBER: 7991-015-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-504-4444
TELEFAX: 215-504-4545
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-108-006C-28

Query Match 50.5%; Score 9.6; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGGATCTCTT 16
DB 17 CCCCACATCTCTT 2

RESULT 26
US-09-422-978-7112
Sequence 7112, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 7112
LENGTH: 19
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..19
OTHER INFORMATION: upstream amplification primer 99-24190 for SEQ 3178.
US-09-422-978-7112

Query Match 50.5%; Score 9.6; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ACGGATCTCTTCAC 19
DB 4 AGGAGTCTCTCCAC 19

RESULT 27
US-09-688-188B-74/C
Sequence 74, Application US/09688188B
Patent No. 6656716
GENERAL INFORMATION:
APPLICANT: PLOMMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 74
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-688-188B-74

Query Match 50.5%; Score 9.6; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGGATCTCTT 16
DB 16 CGCAGCGCATGCTCTT 1

RESULT 28
US-09-291-417D-74/C
Sequence 74, Application US/09291417D
Patent No. 6680170
GENERAL INFORMATION:
APPLICANT: PLOMMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
CURRENT FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14

```
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-291-417D-74
```

```
Query Match          50.5%; Score 9.6; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 CGCAGGTATCTCTTC 16
         |||||
Db       16 CGCAGCGCATGTCCTT 1
```

```
RESULT 29
US-09-544-398B-169/C
; Sequence 169, Application US/09544398B
```

```
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carnelli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 169
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-169
```

```
Query Match          50.5%; Score 9.6; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 GCACGGTATCTCTTC 17
         |||||
Db       19 GCCCTGAATCCTCTT 4
```

```
RESULT 30
US-09-543-771B-169/C
; Sequence 169, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carnelli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
```

```
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 169
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-169
```

```
Query Match          50.5%; Score 9.6; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 GCACGGTATCTCTTC 17
         |||||
Db       19 GCCCTGAATCCTCTT 4
```

```
RESULT 31
US-10-032-495A-20
; Sequence 20, Application US/10032495A
```

```
; Patent No. 7030292
; GENERAL INFORMATION:
; APPLICANT: YAN, MEN LIANG
; TITLE OF INVENTION: METHOD FOR PRODUCING A POPULATION OF HOMOZYGOUS STEM
; TITLE OF INVENTION: CELLS HAVING A PRE-SELECTED IMMUNOTYPE AND/OR GENOTYPE.
; TITLE OF INVENTION: CELLS SUITABLE FOR TRANSPLANT DERIVED THEREFROM, AND
; TITLE OF INVENTION: MATERIALS AND METHODS USING SAME
; FILE REFERENCE: 0249-000205
; CURRENT APPLICATION NUMBER: US/10/032,495A
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 60/258,881
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-032-495A-20
```

```
Query Match          50.5%; Score 9.6; DB 5; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 CGCAGGTATCTCTTC 16
         |||||
Db       3 GCACGGAATCTCTT 18
```

```
RESULT 32
US-09-696-791-3133
; Sequence 3133, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tiltz, Richard
; TITLE OF INVENTION: RIBOSOME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3133
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cyclin A1 ribozyme binding site
US-09-696-791-3133
```

Query Match 49.5%; Score 9.4; DB 3; Length 19;
Best Local Similarity 90.9%; Pred. No. 1.7e+05;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCTTCA 18
Db 1 TTTCTCTTCA 11

RESULT 33

US-09-747-385-7/c
; Sequence 7, Application US/09747385
; Patent No. 6962990
; GENERAL INFORMATION:
; APPLICANT: Attarian, Gwynne
; APPLICANT: Podkaminer, Kara K.
; APPLICANT: Yoder, Sean C.
; APPLICANT: Kinder Haake, Susan A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Psychobacterium Nucleic Acids, Plasmids and Vectors
; FILE REFERENCE: 02307E-099810US
; CURRENT APPLICATION NUMBER: US/09/747,385
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/173,168
; PRIOR FILING DATE: 1999-12-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:rlx
; US-09-747-385-7

Query Match 49.5%; Score 9.4; DB 4; Length 19;
Best Local Similarity 90.9%; Pred. No. 1.7e+05;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 ATCTCTTAC 19
Db 15 ATCTCTTAC 5

RESULT 34

US-09-506-729-1/c
; Sequence 1, Application US/09506729
; Patent No. 6365352
; GENERAL INFORMATION:
; APPLICANT: Yerramilli, Subrahmanyam V.
; APPLICANT: Prashar, Yatindra
; APPLICANT: Newberger, Peter
; APPLICANT: Goguen, Jon
; APPLICANT: Weissen, Sherman M.
; TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
; TITLE OF INVENTION: GRANDLOCYTIC CELLS
; FILE REFERENCE: 44921-5016-US
; CURRENT APPLICATION NUMBER: US/09/506,729
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: PCT/US98/17284
; EARLIER FILING DATE: 1998-08-21
; EARLIER APPLICATION NUMBER: 60/056,844
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-506-729-1

Query Match 48.4%; Score 9.2; DB 3; Length 19;
Best Local Similarity 78.6%; Pred. No. 2.2e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGGATCTCTTCA 18
Db 17 CGGATCTCTTCA 4

RESULT 35

US-09-422-978-5154
; Sequence 5154, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marla
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5154
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-22087 for SEQ 1220,
; US-09-422-978-5154

Query Match 48.4%; Score 9.2; DB 3; Length 19;
Best Local Similarity 78.6%; Pred. No. 2.2e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GGTATCTCTTAC 19
Db 1 GGTATCTCTTAC 14

RESULT 36

US-09-973-132-2
; Sequence 2, Application US/09973132
; Patent No. 6593092
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; APPLICANT: Merchant, B.T.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragments
; US-09-973-132-2

Query Match 48.4%; Score 9.2; DB 3; Length 19;

Best Local Similarity 78.6%; Pred. No. 2.2e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 ACGGATCTCCTTC 17
Db 2 ACGGACGGCCTTC 15

RESULT 37

US-09-696-791-1137
Sequence 1137, Application US/09696791

Patent No. 6770633
GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Trletz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1137
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Cdk-we-hu ribozyme binding site
US-09-696-791-1137

Query Match 48.4%; Score 9.2; DB 3; Length 19;
Best Local Similarity 78.6%; Pred. No. 2.2e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GGTATCTCCTTCAC 19
Db 3 GGTAGCTCTTCTC 16

RESULT 38

US-09-696-791-1138
Sequence 1138, Application US/09696791

Patent No. 6770633
GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Trletz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1138
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Cdk-we-hu ribozyme binding site
US-09-696-791-1138

Query Match 48.4%; Score 9.2; DB 3; Length 19;
Best Local Similarity 78.6%; Pred. No. 2.2e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GGTATCTCCTTCAC 19
Db 1 GGTAGCTCTTCTC 14

RESULT 39

US-09-696-791-1429
Sequence 1429, Application US/09696791

Patent No. 6770633
GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Trletz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1429
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Cyclin A2 ribozyme binding site
US-09-696-791-1429

Query Match 48.4%; Score 9.2; DB 3; Length 19;
Best Local Similarity 78.6%; Pred. No. 2.2e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CACGGTATCTCCTT 16
Db 4 CACGCTTCCTCCTT 17

RESULT 40

US-09-696-791-1430
Sequence 1430, Application US/09696791

Patent No. 6770633
GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Trletz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1430
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Cyclin A2 ribozyme binding site
US-09-696-791-1430

Query Match 48.4%; Score 9.2; DB 3; Length 19;
Best Local Similarity 78.6%; Pred. No. 2.2e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CACGGTATCTCCTT 16
Db 3 CACGCTTCCTCCTT 16

Search completed: August 10, 2006, 09:00:57
Job time : 111.333 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 08:47:46 ; Search time 625.333 Seconds
(without alignment)
373.345 Million cell updates/sec

Title: US-10-636-065-29

Perfect score: 19
Sequence: 1 cgcacgctactcttcac 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 segs, 6143817638 residues

Total number of hits satisfying chosen parameters: 6941248

Minimum DB seq length: 19
Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Databases :

Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US09_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US09C_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10C_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	8	US-10-636-065-29
2	14.4	75.8	19	14	US-11-083-784-787223
3	14.4	75.8	19	15	US-11-101-244-787223
4	14	73.7	19	7	US-10-400-382-29
5	14	73.7	19	7	US-10-400-382-107
6	14	73.7	19	10	US-10-975-790-29
7	14	73.7	19	10	US-10-975-790-107
8	13.4	70.5	19	14	US-11-083-784-796889
9	13.4	70.5	19	15	US-11-101-244-796889
10	13	68.4	19	10	US-10-739-904-10
11	13	68.4	19	14	US-11-083-784-1156068
12	13	68.4	19	15	US-11-101-244-1156068
13	12.8	67.4	19	14	US-11-083-784-224158
14	12.8	67.4	19	14	US-11-083-784-761475
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16	12.8	67.4	19	15	US-11-101-244-761475
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19	12.4	65.3	19	14	US-11-083-784-183913	Sequence 183913,
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21	12.4	65.3	19	14	US-11-083-784-475145	Sequence 475145,
22	12.4	65.3	19	14	US-11-083-784-475149	Sequence 475149,
23	12.4	65.3	19	14	US-11-083-784-583673	Sequence 583673,
24	12.4	65.3	19	14	US-11-083-784-796832	Sequence 796832,
25	12.4	65.3	19	14	US-11-083-784-796832	Sequence 796832,
26	12.4	65.3	19	14	US-11-083-784-1087813	Sequence 1087813,
27	12.4	65.3	19	14	US-11-083-784-1087813	Sequence 1087813,
28	12.4	65.3	19	14	US-11-083-784-1180480	Sequence 1180480,
29	12.4	65.3	19	14	US-11-083-784-1191739	Sequence 1191739,
30	12.4	65.3	19	14	US-11-083-784-1191772	Sequence 1191772,
31	12.4	65.3	19	14	US-11-083-784-1306236	Sequence 1306236,
32	12.4	65.3	19	14	US-11-083-784-1585329	Sequence 1585329,
33	12.4	65.3	19	14	US-11-083-784-1585348	Sequence 1585348,
34	12.4	65.3	19	15	US-11-101-244-754	Sequence 754, App
35	12.4	65.3	19	15	US-11-101-244-183913	Sequence 183913,
36	12.4	65.3	19	15	US-11-101-244-222011	Sequence 222011,
37	12.4	65.3	19	15	US-11-101-244-475145	Sequence 475145,
38	12.4	65.3	19	15	US-11-101-244-475149	Sequence 475149,
39	12.4	65.3	19	15	US-11-101-244-583673	Sequence 583673,
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43	12.4	65.3	19	15	US-11-101-244-1087813	Sequence 1087813,
44	12.4	65.3	19	15	US-11-101-244-1180480	Sequence 1180480,
45	12.4	65.3	19	15	US-11-101-244-1191739	Sequence 1191739,
46	12.4	65.3	19	15	US-11-101-244-1191772	Sequence 1191772,
47	12.4	65.3	19	15	US-11-101-244-1306236	Sequence 1306236,
48	12.4	65.3	19	15	US-11-101-244-1585329	Sequence 1585329,
49	12.4	65.3	19	15	US-11-101-244-1585348	Sequence 1585348,
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51	12.2	64.2	19	11	US-10-636-598-33	Sequence 33, Appl
52	12.2	64.2	19	14	US-11-083-784-62682	Sequence 62682, A
53	12.2	64.2	19	14	US-11-083-784-80634	Sequence 80634, A
54	12.2	64.2	19	14	US-11-083-784-193376	Sequence 193376,
55	12.2	64.2	19	14	US-11-083-784-273138	Sequence 273138,
56	12.2	64.2	19	14	US-11-083-784-274885	Sequence 274885,
57	12.2	64.2	19	14	US-11-083-784-343449	Sequence 343449,
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59	12.2	64.2	19	14	US-11-083-784-472120	Sequence 472120,
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61	12.2	64.2	19	14	US-11-083-784-518183	Sequence 518183,
62	12.2	64.2	19	14	US-11-083-784-648223	Sequence 648223,
63	12.2	64.2	19	14	US-11-083-784-972359	Sequence 972359,
64	12.2	64.2	19	14	US-11-083-784-1036216	Sequence 1036216,
65	12.2	64.2	19	14	US-11-083-784-1170322	Sequence 1170322,
66	12.2	64.2	19	14	US-11-083-784-1516953	Sequence 1516953,
67	12.2	64.2	19	15	US-11-101-244-62682	Sequence 62682, A
68	12.2	64.2	19	15	US-11-101-244-80634	Sequence 80634, A
69	12.2	64.2	19	15	US-11-101-244-193376	Sequence 193376,
70	12.2	64.2	19	15	US-11-101-244-273138	Sequence 273138,
71	12.2	64.2	19	15	US-11-101-244-274885	Sequence 274885,
72	12.2	64.2	19	15	US-11-101-244-343449	Sequence 343449,
73	12.2	64.2	19	15	US-11-101-244-472120	Sequence 472120,
74	12.2	64.2	19	15	US-11-101-244-472125	Sequence 472125,
75	12.2	64.2	19	15	US-11-101-244-518183	Sequence 518183,
76	12.2	64.2	19	15	US-11-101-244-648223	Sequence 648223,
77	12.2	64.2	19	15	US-11-101-244-972359	Sequence 972359,
78	12.2	64.2	19	15	US-11-101-244-1036216	Sequence 1036216,
79	12.2	64.2	19	15	US-11-101-244-1170322	Sequence 1170322,
80	12.2	64.2	19	15	US-11-101-244-1516953	Sequence 1516953,
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82	12.2	64.2	19	15	US-11-101-244-80634	Sequence 80634, A
83	12.2	64.2	19	15	US-11-101-244-193376	Sequence 193376,
84	12.2	64.2	19	15	US-11-101-244-273138	Sequence 273138,
85	12.2	64.2	19	15	US-11-101-244-274885	Sequence 274885,
86	12.2	64.2	19	15	US-11-101-244-343449	Sequence 343449,
87	12.2	64.2	19	15	US-11-101-244-472120	Sequence 472120,
88	12.2	64.2	19	15	US-11-101-244-472125	Sequence 472125,
89	12.2	64.2	19	15	US-11-101-244-518183	Sequence 518183,
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92	12	63.2	617342	19	15	US-11-101-244-617342	Sequence 617342,
93	12	63.2	775182	19	15	US-11-101-244-775182	Sequence 775182,
C 94	12	63.2	873317	19	15	US-11-101-244-873317	Sequence 873317,
95	12	63.2	940223	19	15	US-11-101-244-940223	Sequence 940223,
C 96	12	63.2	1190154	19	15	US-11-101-244-1190154	Sequence 1190154,
C 97	12	63.2	1499582	19	15	US-11-101-244-1499582	Sequence 1499582,
C 98	12	63.2	628444	19	15	US-10-310-914A-628444	Sequence 628444,
99	11.8	62.1	1026980	19	11	US-10-310-914A-1026980	Sequence 1026980,
C 100	11.8	62.1	43373	19	14	US-11-083-784-43373	Sequence 43373, A
C 101	11.8	62.1	43424	19	14	US-11-083-784-43424	Sequence 43424, A
C 102	11.8	62.1	227032	19	14	US-11-083-784-227032	Sequence 227032,
C 103	11.8	62.1	267464	19	14	US-11-083-784-267464	Sequence 267464,
C 104	11.8	62.1	267569	19	14	US-11-083-784-267569	Sequence 267569,
C 105	11.8	62.1	267671	19	14	US-11-083-784-267671	Sequence 267671,
C 106	11.8	62.1	267773	19	14	US-11-083-784-267773	Sequence 267773,
C 107	11.8	62.1	267877	19	14	US-11-083-784-267877	Sequence 267877,
C 108	11.8	62.1	417171	19	14	US-11-083-784-417171	Sequence 417171,
C 109	11.8	62.1	507577	19	14	US-11-083-784-507577	Sequence 507577,
C 110	11.8	62.1	518698	19	14	US-11-083-784-518698	Sequence 518698,
C 111	11.8	62.1	532240	19	14	US-11-083-784-532240	Sequence 532240,
C 112	11.8	62.1	532339	19	14	US-11-083-784-532339	Sequence 532339,
C 113	11.8	62.1	535700	19	14	US-11-083-784-535700	Sequence 535700,
C 114	11.8	62.1	535731	19	14	US-11-083-784-535731	Sequence 535731,
C 115	11.8	62.1	535890	19	14	US-11-083-784-535890	Sequence 535890,
C 116	11.8	62.1	535926	19	14	US-11-083-784-535926	Sequence 535926,
C 117	11.8	62.1	535975	19	14	US-11-083-784-535975	Sequence 535975,
C 118	11.8	62.1	728588	19	14	US-11-083-784-728588	Sequence 728588,
C 119	11.8	62.1	728818	19	14	US-11-083-784-728818	Sequence 728818,
C 120	11.8	62.1	928077	19	14	US-11-083-784-928077	Sequence 928077,
C 121	11.8	62.1	928179	19	14	US-11-083-784-928179	Sequence 928179,
C 122	11.8	62.1	978926	19	14	US-11-083-784-978926	Sequence 978926,
C 123	11.8	62.1	978974	19	14	US-11-083-784-978974	Sequence 978974,
C 124	11.8	62.1	979023	19	14	US-11-083-784-979023	Sequence 979023,
C 125	11.8	62.1	979077	19	14	US-11-083-784-979077	Sequence 979077,
C 126	11.8	62.1	1085058	19	14	US-11-083-784-1085058	Sequence 1085058,
C 127	11.8	62.1	1091023	19	14	US-11-083-784-1091023	Sequence 1091023,
C 128	11.8	62.1	1138508	19	14	US-11-083-784-1138508	Sequence 1138508,
C 129	11.8	62.1	1270102	19	14	US-11-083-784-1270102	Sequence 1270102,
C 130	11.8	62.1	1305551	19	14	US-11-083-784-1305551	Sequence 1305551,
C 131	11.8	62.1	1327567	19	14	US-11-083-784-1327567	Sequence 1327567,
C 132	11.8	62.1	1379186	19	14	US-11-083-784-1379186	Sequence 1379186,
C 133	11.8	62.1	1450500	19	14	US-11-083-784-1450500	Sequence 1450500,
C 134	11.8	62.1	1484872	19	14	US-11-083-784-1484872	Sequence 1484872,
C 135	11.8	62.1	1485014	19	14	US-11-083-784-1485014	Sequence 1485014,
C 136	11.8	62.1	1516898	19	14	US-11-083-784-1516898	Sequence 1516898,
C 137	11.8	62.1	43373	19	15	US-11-101-244-43373	Sequence 43373, A
C 138	11.8	62.1	43424	19	15	US-11-101-244-43424	Sequence 43424, A
C 139	11.8	62.1	227032	19	15	US-11-101-244-227032	Sequence 227032,
C 140	11.8	62.1	267464	19	15	US-11-101-244-267464	Sequence 267464,
C 141	11.8	62.1	267569	19	15	US-11-101-244-267569	Sequence 267569,
C 142	11.8	62.1	267671	19	15	US-11-101-244-267671	Sequence 267671,
C 143	11.8	62.1	267773	19	15	US-11-101-244-267773	Sequence 267773,
C 144	11.8	62.1	267877	19	15	US-11-101-244-267877	Sequence 267877,
C 145	11.8	62.1	417171	19	15	US-11-101-244-417171	Sequence 417171,
C 146	11.8	62.1	507577	19	15	US-11-101-244-507577	Sequence 507577,
C 147	11.8	62.1	518698	19	15	US-11-101-244-518698	Sequence 518698,
C 148	11.8	62.1	532240	19	15	US-11-101-244-532240	Sequence 532240,
C 149	11.8	62.1	532339	19	15	US-11-101-244-532339	Sequence 532339,
C 150	11.8	62.1	535700	19	15	US-11-101-244-535700	Sequence 535700,
C 151	11.8	62.1	535731	19	15	US-11-101-244-535731	Sequence 535731,
C 152	11.8	62.1	535890	19	15	US-11-101-244-535890	Sequence 535890,
C 153	11.8	62.1	535926	19	15	US-11-101-244-535926	Sequence 535926,
C 154	11.8	62.1	535975	19	15	US-11-101-244-535975	Sequence 535975,
C 155	11.8	62.1	728588	19	15	US-11-101-244-728588	Sequence 728588,
C 156	11.8	62.1	728818	19	15	US-11-101-244-728818	Sequence 728818,
C 157	11.8	62.1	928077	19	15	US-11-101-244-928077	Sequence 928077,
C 158	11.8	62.1	928179	19	15	US-11-101-244-928179	Sequence 928179,
C 159	11.8	62.1	978926	19	15	US-11-101-244-978926	Sequence 978926,
C 160	11.8	62.1	978974	19	15	US-11-101-244-978974	Sequence 978974,
C 161	11.8	62.1	979023	19	15	US-11-101-244-979023	Sequence 979023,
C 162	11.8	62.1	979077	19	15	US-11-101-244-979077	Sequence 979077,
C 163	11.8	62.1	1085058	19	15	US-11-101-244-1085058	Sequence 1085058,

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240	11.4	60.0	19	14	US-11-083-784-1020279	Sequence 1020279,	313	11.2	58.9	19	11	US-10-310-914A-1173006	Sequence 1173006,
241	11.4	60.0	19	14	US-11-083-784-1041213	Sequence 1041213,	314	11.2	58.9	19	11	US-10-310-914A-1301564	Sequence 1301564,
242	11.4	60.0	19	14	US-11-083-784-1108242	Sequence 1108242,	315	11.2	58.9	19	14	US-11-083-784-7839	Sequence 7839, Ap
243	11.4	60.0	19	14	US-11-083-784-1108324	Sequence 1108324,	316	11.2	58.9	19	14	US-11-083-784-7897	Sequence 7897, Ap
244	11.4	60.0	19	14	US-11-083-784-1179079	Sequence 1179079,	317	11.2	58.9	19	14	US-11-083-784-20131	Sequence 20131, A
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246	11.4	60.0	19	14	US-11-083-784-1370161	Sequence 1370161,	319	11.2	58.9	19	14	US-11-083-784-51229	Sequence 51229, A
247	11.4	60.0	19	14	US-11-083-784-1415850	Sequence 1415850,	320	11.2	58.9	19	14	US-11-083-784-65414	Sequence 65414, A
248	11.4	60.0	19	14	US-11-083-784-1480947	Sequence 1480947,	321	11.2	58.9	19	14	US-11-083-784-93455	Sequence 93455, A
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250	11.4	60.0	19	14	US-11-083-784-1516923	Sequence 1516923,	323	11.2	58.9	19	14	US-11-083-784-118842	Sequence 118842,
251	11.4	60.0	19	14	US-11-083-784-1526480	Sequence 1526480,	324	11.2	58.9	19	14	US-11-083-784-120268	Sequence 120268,
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258	11.4	60.0	19	15	US-11-101-244-31451	Sequence 31451, A	331	11.2	58.9	19	14	US-11-083-784-224276	Sequence 224276,
259	11.4	60.0	19	15	US-11-101-244-48400	Sequence 48400, A	332	11.2	58.9	19	14	US-11-083-784-236018	Sequence 236018,
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262	11.4	60.0	19	15	US-11-101-244-185363	Sequence 185363,	335	11.2	58.9	19	14	US-11-083-784-384640	Sequence 384640,
263	11.4	60.0	19	15	US-11-101-244-185364	Sequence 185364,	336	11.2	58.9	19	14	US-11-083-784-389290	Sequence 389290,
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265	11.4	60.0	19	15	US-11-101-244-237456	Sequence 237456,	338	11.2	58.9	19	14	US-11-083-784-518161	Sequence 518161,
266	11.4	60.0	19	15	US-11-101-244-249818	Sequence 249818,	339	11.2	58.9	19	14	US-11-083-784-537696	Sequence 537696,
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281	11.4	60.0	19	15	US-11-101-244-854864	Sequence 854864,	354	11.2	58.9	19	14	US-11-083-784-808982	Sequence 808982,
282	11.4	60.0	19	15	US-11-101-244-944650	Sequence 944650,	355	11.2	58.9	19	14	US-11-083-784-823362	Sequence 823362,
283	11.4	60.0	19	15	US-11-101-244-944734	Sequence 944734,	356	11.2	58.9	19	14	US-11-083-784-856423	Sequence 856423,
284	11.4	60.0	19	15	US-11-101-244-944849	Sequence 944849,	357	11.2	58.9	19	14	US-11-083-784-873164	Sequence 873164,
285	11.4	60.0	19	15	US-11-101-244-944950	Sequence 944950,	358	11.2	58.9	19	14	US-11-083-784-880982	Sequence 880982,
286	11.4	60.0	19	15	US-11-101-244-945051	Sequence 945051,	359	11.2	58.9	19	14	US-11-083-784-919024	Sequence 919024,
287	11.4	60.0	19	15	US-11-101-244-967894	Sequence 967894,	360	11.2	58.9	19	14	US-11-083-784-974315	Sequence 974315,
288	11.4	60.0	19	15	US-11-101-244-1020235	Sequence 1020235,	361	11.2	58.9	19	14	US-11-083-784-985475	Sequence 985475,
289	11.4	60.0	19	15	US-11-101-244-1020262	Sequence 1020262,	362	11.2	58.9	19	14	US-11-083-784-1036215	Sequence 1036215,
290	11.4	60.0	19	15	US-11-101-244-1020268	Sequence 1020268,	363	11.2	58.9	19	14	US-11-083-784-1043139	Sequence 1043139,
291	11.4	60.0	19	15	US-11-101-244-1020269	Sequence 1020269,	364	11.2	58.9	19	14	US-11-083-784-1071039	Sequence 1071039,
292	11.4	60.0	19	15	US-11-101-244-1020279	Sequence 1020279,	365	11.2	58.9	19	14	US-11-083-784-1291821	Sequence 1291821,
293	11.4	60.0	19	15	US-11-101-244-1041213	Sequence 1041213,	366	11.2	58.9	19	14	US-11-083-784-1112807	Sequence 1112807,
294	11.4	60.0	19	15	US-11-101-244-1108324	Sequence 1108324,	367	11.2	58.9	19	14	US-11-083-784-1112807	Sequence 1112807,
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298	11.4	60.0	19	15	US-11-101-244-1370161	Sequence 1370161,	371	11.2	58.9	19	14	US-11-083-784-1121360	Sequence 1121360,
299	11.4	60.0	19	15	US-11-101-244-1415850	Sequence 1415850,	372	11.2	58.9	19	14	US-11-083-784-1171715	Sequence 1171715,
300	11.4	60.0	19	15	US-11-101-244-1415850	Sequence 1415850,	373	11.2	58.9	19	14	US-11-083-784-1171715	Sequence 1171715,
301	11.4	60.0	19	15	US-11-101-244-1507475	Sequence 1507475,	374	11.2	58.9	19	14	US-11-083-784-1209251	Sequence 1209251,
302	11.4	60.0	19	15	US-11-101-244-1516923	Sequence 1516923,	375	11.2	58.9	19	14	US-11-083-784-1209251	Sequence 1209251,
303	11.4	60.0	19	15	US-11-101-244-1526480	Sequence 1526480,	376	11.2	58.9	19	14	US-11-083-784-1281866	Sequence 1281866,
304	11.4	60.0	19	15	US-11-101-244-1531886	Sequence 1531886,	377	11.2	58.9	19	14	US-11-083-784-1291821	Sequence 1291821,
305	11.4	60.0	19	15	US-11-101-244-1586384	Sequence 1586384,	378	11.2	58.9	19	14	US-11-083-784-1293500	Sequence 1293500,
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309	11.2	58.9	19	11	US-10-310-914A-366185	Sequence 366185,	382	11.2	58.9	19	14	US-11-083-784-1449808	Sequence 1449808,

383	11.2	58.9	19	14	US-11-083-784-1481525	Sequence 1481525,
384	11.2	58.9	19	14	US-11-083-784-1558682	Sequence 1558682,
385	11.2	58.9	19	14	US-11-083-784-1567299	Sequence 1567299,
386	11.2	58.9	19	14	US-11-083-784-1589489	Sequence 1589489,
387	11.2	58.9	19	14	US-11-083-784-1589494	Sequence 1589494,
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389	11.2	58.9	19	15	US-11-101-244-7897	Sequence 7897, Ap
390	11.2	58.9	19	15	US-11-101-244-20131	Sequence 20131, A
391	11.2	58.9	19	15	US-11-101-244-30759	Sequence 30759, A
392	11.2	58.9	19	15	US-11-101-244-51529	Sequence 51529, A
393	11.2	58.9	19	15	US-11-101-244-65414	Sequence 65414, A
394	11.2	58.9	19	15	US-11-101-244-93455	Sequence 93455, A
395	11.2	58.9	19	15	US-11-101-244-96080	Sequence 96080, A
396	11.2	58.9	19	15	US-11-101-244-118842	Sequence 118842,
397	11.2	58.9	19	15	US-11-101-244-120268	Sequence 120268,
398	11.2	58.9	19	15	US-11-101-244-146722	Sequence 146722,
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403	11.2	58.9	19	15	US-11-101-244-224244	Sequence 224244,
404	11.2	58.9	19	15	US-11-101-244-224276	Sequence 224276,
405	11.2	58.9	19	15	US-11-101-244-236018	Sequence 236018,
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407	11.2	58.9	19	15	US-11-101-244-277905	Sequence 277905,
408	11.2	58.9	19	15	US-11-101-244-325875	Sequence 325875,
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412	11.2	58.9	19	15	US-11-101-244-518161	Sequence 518161,
413	11.2	58.9	19	15	US-11-101-244-537696	Sequence 537696,
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415	11.2	58.9	19	15	US-11-101-244-587302	Sequence 587302,
416	11.2	58.9	19	15	US-11-101-244-587315	Sequence 587315,
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423	11.2	58.9	19	15	US-11-101-244-744868	Sequence 744868,
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453	11.2	58.9	19	15	US-11-101-244-1342570	Sequence 1342570,
454	11.2	58.9	19	15	US-11-101-244-1449798	Sequence 1449798,
455	11.2	58.9	19	15	US-11-101-244-1449808	Sequence 1449808,
456	11.2	58.9	19	15	US-11-101-244-1481525	Sequence 1481525,
457	11.2	58.9	19	15	US-11-101-244-1558682	Sequence 1558682,
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463	11.2	58.9	19	10	US-10-671-883-43	Sequence 43, Ap1
464	11.2	58.9	19	10	US-10-864-044-39	Sequence 39, Ap1
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468	11.2	58.9	19	11	US-10-310-914A-1333076	Sequence 1323076,
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470	11.2	58.9	19	14	US-11-083-784-40450	Sequence 40450, A
471	11.2	58.9	19	14	US-11-083-784-764172	Sequence 76412, A
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473	11.2	58.9	19	14	US-11-083-784-112575	Sequence 112575,
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476	11.2	58.9	19	14	US-11-083-784-165170	Sequence 165170,
477	11.2	58.9	19	14	US-11-083-784-165273	Sequence 165273,
478	11.2	58.9	19	14	US-11-083-784-165373	Sequence 165373,
479	11.2	58.9	19	14	US-11-083-784-165483	Sequence 165483,
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483	11.2	58.9	19	14	US-11-083-784-415594	Sequence 415594,
484	11.2	58.9	19	14	US-11-083-784-415625	Sequence 415625,
485	11.2	58.9	19	14	US-11-083-784-442137	Sequence 442137,
486	11.2	58.9	19	14	US-11-083-784-447063	Sequence 447063,
487	11.2	58.9	19	14	US-11-083-784-473387	Sequence 473387,
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503	11.2	58.9	19	14	US-11-083-784-877308	Sequence 877308,
504	11.2	58.9	19	14	US-11-083-784-877409	Sequence 877409,
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523	11.2	58.9	19	14	US-11-083-784-1344077	Sequence 1344077,
524	11.2	58.9	19	14	US-11-083-784-1379512	Sequence 1379512,
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527	11.2	58.9	19	14	US-11-083-784-1391776	Sequence 1391776,
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C 529	11	57.9	19	14	US-11-083-784-1394923	Sequence 1394923,	C 602	11	57.9	19	15	US-11-101-244-1569410	Sequence 1569410,
C 530	11	57.9	19	14	US-11-083-784-1394946	Sequence 1394946,	C 603	11	57.9	19	15	US-11-110-011-23	Sequence 23, App1
C 531	11	57.9	19	14	US-11-083-784-1415916	Sequence 1415916,	C 604	10.8	56.8	19	7	US-10-251-117-625	Sequence 626, App
C 532	11	57.9	19	14	US-11-083-784-1487768	Sequence 1487768,	C 605	10.8	56.8	19	7	US-10-251-117-933	Sequence 933, App
C 533	11	57.9	19	14	US-11-083-784-1538882	Sequence 1538882,	C 606	10.8	56.8	19	10	US-10-923-354-572	Sequence 572, App
C 534	11	57.9	19	14	US-11-083-784-1545060	Sequence 1545060,	C 607	10.8	56.8	19	11	US-10-923-354-879	Sequence 879, App
C 535	11	57.9	19	14	US-11-083-784-1559410	Sequence 1559410,	C 608	10.8	56.8	19	11	US-10-310-914A-44955	Sequence 44955, A
C 536	11	57.9	19	15	US-11-101-244-753	Sequence 753, App	C 609	10.8	56.8	19	11	US-10-310-914A-56001	Sequence 56001, A
C 537	11	57.9	19	15	US-11-101-244-40450	Sequence 40450, A	C 610	10.8	56.8	19	11	US-10-310-914A-62832	Sequence 62832,
C 538	11	57.9	19	15	US-11-101-244-76412	Sequence 76412, A	C 611	10.8	56.8	19	11	US-10-310-914A-1106388	Sequence 1106388,
C 539	11	57.9	19	15	US-11-101-244-93476	Sequence 93476, A	C 612	10.8	56.8	19	11	US-10-310-914A-1106627	Sequence 1106627,
C 540	11	57.9	19	15	US-11-101-244-112575	Sequence 112575,	C 613	10.8	56.8	19	14	US-10-310-914A-1159114	Sequence 1159114,
C 541	11	57.9	19	15	US-11-101-244-112811	Sequence 112811,	C 614	10.8	56.8	19	14	US-11-083-784-880	Sequence 880, App
C 542	11	57.9	19	15	US-11-101-244-165071	Sequence 165071,	C 615	10.8	56.8	19	14	US-11-083-784-15392	Sequence 15392, App
C 543	11	57.9	19	15	US-11-101-244-165170	Sequence 165170,	C 616	10.8	56.8	19	14	US-11-083-784-17547	Sequence 17457, A
C 544	11	57.9	19	15	US-11-101-244-165273	Sequence 165273,	C 617	10.8	56.8	19	14	US-11-083-784-17554	Sequence 17554, A
C 545	11	57.9	19	15	US-11-101-244-165373	Sequence 165373,	C 618	10.8	56.8	19	14	US-11-083-784-17566	Sequence 17656, A
C 546	11	57.9	19	15	US-11-101-244-165483	Sequence 165483,	C 619	10.8	56.8	19	14	US-11-083-784-17755	Sequence 17855, A
C 547	11	57.9	19	15	US-11-101-244-185350	Sequence 185350,	C 620	10.8	56.8	19	14	US-11-083-784-17855	Sequence 17856, A
C 548	11	57.9	19	15	US-11-101-244-222010	Sequence 222010,	C 621	10.8	56.8	19	14	US-11-083-784-17955	Sequence 17955, A
C 549	11	57.9	19	15	US-11-101-244-415574	Sequence 415574,	C 622	10.8	56.8	19	14	US-11-083-784-17955	Sequence 17956, A
C 550	11	57.9	19	15	US-11-101-244-415594	Sequence 415594,	C 623	10.8	56.8	19	14	US-11-083-784-63811	Sequence 63811, A
C 551	11	57.9	19	15	US-11-101-244-415625	Sequence 415625,	C 624	10.8	56.8	19	14	US-11-083-784-63911	Sequence 63911, A
C 552	11	57.9	19	15	US-11-101-244-442137	Sequence 442137,	C 625	10.8	56.8	19	14	US-11-083-784-102948	Sequence 102948,
C 553	11	57.9	19	15	US-11-101-244-473387	Sequence 473387,	C 626	10.8	56.8	19	14	US-11-083-784-103044	Sequence 103044,
C 554	11	57.9	19	15	US-11-101-244-509990	Sequence 509990,	C 627	10.8	56.8	19	14	US-11-083-784-16721	Sequence 16721,
C 555	11	57.9	19	15	US-11-101-244-518167	Sequence 518167,	C 628	10.8	56.8	19	14	US-11-083-784-152794	Sequence 152794,
C 556	11	57.9	19	15	US-11-101-244-518944	Sequence 518944,	C 629	10.8	56.8	19	14	US-11-083-784-152799	Sequence 152817,
C 557	11	57.9	19	15	US-11-101-244-559809	Sequence 559809,	C 630	10.8	56.8	19	14	US-11-083-784-152817	Sequence 152817,
C 558	11	57.9	19	15	US-11-101-244-633006	Sequence 633006,	C 631	10.8	56.8	19	14	US-11-083-784-152427	Sequence 152427,
C 559	11	57.9	19	15	US-11-101-244-643216	Sequence 643216,	C 632	10.8	56.8	19	14	US-11-083-784-157546	Sequence 157546,
C 560	11	57.9	19	15	US-11-101-244-643267	Sequence 643267,	C 633	10.8	56.8	19	14	US-11-083-784-16525	Sequence 16525,
C 561	11	57.9	19	15	US-11-101-244-643640	Sequence 643640,	C 634	10.8	56.8	19	14	US-11-083-784-165616	Sequence 165616,
C 562	11	57.9	19	15	US-11-101-244-645671	Sequence 645671,	C 635	10.8	56.8	19	14	US-11-083-784-202557	Sequence 202557,
C 563	11	57.9	19	15	US-11-101-244-666334	Sequence 666334,	C 636	10.8	56.8	19	14	US-11-083-784-224249	Sequence 224249,
C 564	11	57.9	19	15	US-11-101-244-666398	Sequence 666398,	C 637	10.8	56.8	19	14	US-11-083-784-240402	Sequence 240402,
C 565	11	57.9	19	15	US-11-101-244-669383	Sequence 669383,	C 638	10.8	56.8	19	14	US-11-083-784-241175	Sequence 241175,
C 566	11	57.9	19	15	US-11-101-244-669428	Sequence 669428,	C 639	10.8	56.8	19	14	US-11-083-784-241175	Sequence 241175,
C 567	11	57.9	19	15	US-11-101-244-738979	Sequence 738979,	C 640	10.8	56.8	19	14	US-11-083-784-267607	Sequence 267607,
C 568	11	57.9	19	15	US-11-101-244-813149	Sequence 813149,	C 641	10.8	56.8	19	14	US-11-083-784-267607	Sequence 267607,
C 569	11	57.9	19	15	US-11-101-244-877308	Sequence 877308,	C 642	10.8	56.8	19	14	US-11-083-784-267607	Sequence 267607,
C 570	11	57.9	19	15	US-11-101-244-877409	Sequence 877409,	C 643	10.8	56.8	19	14	US-11-083-784-267607	Sequence 267607,
C 571	11	57.9	19	15	US-11-101-244-877409	Sequence 877409,	C 644	10.8	56.8	19	14	US-11-083-784-267607	Sequence 267607,
C 572	11	57.9	19	15	US-11-101-244-878601	Sequence 878601,	C 645	10.8	56.8	19	14	US-11-083-784-267607	Sequence 267607,
C 573	11	57.9	19	15	US-11-101-244-977457	Sequence 977457,	C 646	10.8	56.8	19	14	US-11-083-784-267607	Sequence 267607,
C 574	11	57.9	19	15	US-11-101-244-977466	Sequence 977466,	C 647	10.8	56.8	19	14	US-11-083-784-267607	Sequence 267607,
C 575	11	57.9	19	15	US-11-101-244-1028639	Sequence 1028639,	C 648	10.8	56.8	19	14	US-11-083-784-267607	Sequence 267607,
C 576	11	57.9	19	15	US-11-101-244-1033199	Sequence 1033199,	C 649	10.8	56.8	19	14	US-11-083-784-267607	Sequence 267607,
C 577	11	57.9	19	15	US-11-101-244-1033207	Sequence 1033207,	C 650	10.8	56.8	19	14	US-11-083-784-267607	Sequence 267607,
C 578	11	57.9	19	15	US-11-101-244-1033214	Sequence 1033214,	C 651	10.8	56.8	19	14	US-11-083-784-324131	Sequence 324131,
C 579	11	57.9	19	15	US-11-101-244-1037013	Sequence 1037013,	C 652	10.8	56.8	19	14	US-11-083-784-324232	Sequence 324232,
C 580	11	57.9	19	15	US-11-101-244-1041053	Sequence 1041053,	C 653	10.8	56.8	19	14	US-11-083-784-325880	Sequence 325880,
C 581	11	57.9	19	15	US-11-101-244-1137591	Sequence 1137591,	C 654	10.8	56.8	19	14	US-11-083-784-325925	Sequence 325925,
C 582	11	57.9	19	15	US-11-101-244-1156298	Sequence 1156298,	C 655	10.8	56.8	19	14	US-11-083-784-325925	Sequence 325925,
C 583	11	57.9	19	15	US-11-101-244-1164064	Sequence 1164064,	C 656	10.8	56.8	19	14	US-11-083-784-326510	Sequence 326510,
C 584	11	57.9	19	15	US-11-101-244-1206330	Sequence 1206330,	C 657	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 585	11	57.9	19	15	US-11-101-244-1206338	Sequence 1206338,	C 658	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 586	11	57.9	19	15	US-11-101-244-1206333	Sequence 1206333,	C 659	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 587	11	57.9	19	15	US-11-101-244-1293077	Sequence 1293077,	C 660	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 588	11	57.9	19	15	US-11-101-244-1305606	Sequence 1305606,	C 661	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 589	11	57.9	19	15	US-11-101-244-1326818	Sequence 1326818,	C 662	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 590	11	57.9	19	15	US-11-101-244-1344077	Sequence 1344077,	C 663	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 591	11	57.9	19	15	US-11-101-244-1379512	Sequence 1379512,	C 664	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 592	11	57.9	19	15	US-11-101-244-1388389	Sequence 1388389,	C 665	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 593	11	57.9	19	15	US-11-101-244-1391731	Sequence 1391731,	C 666	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 594	11	57.9	19	15	US-11-101-244-1391776	Sequence 1391776,	C 667	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 595	11	57.9	19	15	US-11-101-244-1391807	Sequence 1391807,	C 668	10.8	56.8	19	14	US-11-083-784-434672	Sequence 434672,
C 596	11	57.9	19	15	US-11-101-244-1394923	Sequence 1394923,	C 669	10.8	56.8	19	14	US-11-083-784-434672	Sequence 434672,
C 597	11	57.9	19	15	US-11-101-244-1394936	Sequence 1394936,	C 670	10.8	56.8	19	14	US-11-083-784-434672	Sequence 434672,
C 598	11	57.9	19	15	US-11-101-244-1415916	Sequence 1415916,	C 671	10.8	56.8	19	14	US-11-083-784-469666	Sequence 469666,
C 599	11	57.9	19	15	US-11-101-244-1487768	Sequence 1487768,	C 672	10.8	56.8	19	14	US-11-083-784-469666	Sequence 469666,
C 600	11	57.9	19	15	US-11-101-244-1538882	Sequence 1538882,	C 673	10.8	56.8	19	14	US-11-083-784-469666	Sequence 469666,
C 601	11	57.9	19	15	US-11-101-244-1545060	Sequence 1545060,	C 674	10.8	56.8	19	14	US-11-083-784-486076	Sequence 486076,

C 675	10.8	56.8	19	14	US-11-083-784-486104	Sequence 486104,	C 748	10.8	56.8	19	14	US-11-083-784-1277890	Sequence 1277890,
C 676	10.8	56.8	19	14	US-11-083-784-486136	Sequence 486136,	C 749	10.8	56.8	19	14	US-11-083-784-1277922	Sequence 1277922,
C 677	10.8	56.8	19	14	US-11-083-784-501009	Sequence 501009,	C 750	10.8	56.8	19	14	US-11-083-784-1281531	Sequence 1281531,
C 678	10.8	56.8	19	14	US-11-083-784-505436	Sequence 505436	C 751	10.8	56.8	19	14	US-11-083-784-1305609	Sequence 1305609,
C 679	10.8	56.8	19	14	US-11-083-784-513499	Sequence 513499,	C 752	10.8	56.8	19	14	US-11-083-784-1330468	Sequence 1330468,
C 680	10.8	56.8	19	14	US-11-083-784-513502	Sequence 513502,	C 753	10.8	56.8	19	14	US-11-083-784-1330474	Sequence 1330474,
C 681	10.8	56.8	19	14	US-11-083-784-553705	Sequence 553705,	C 754	10.8	56.8	19	14	US-11-083-784-1351416	Sequence 1351416,
C 682	10.8	56.8	19	14	US-11-083-784-554055	Sequence 554055,	C 755	10.8	56.8	19	14	US-11-083-784-1351420	Sequence 1351420,
C 683	10.8	56.8	19	14	US-11-083-784-568816	Sequence 568816,	C 756	10.8	56.8	19	14	US-11-083-784-1351433	Sequence 1351433,
C 684	10.8	56.8	19	14	US-11-083-784-568927	Sequence 568927,	C 757	10.8	56.8	19	14	US-11-083-784-1395315	Sequence 1395315,
C 685	10.8	56.8	19	14	US-11-083-784-572332	Sequence 572332,	C 758	10.8	56.8	19	14	US-11-083-784-1395853	Sequence 1395853,
C 686	10.8	56.8	19	14	US-11-083-784-572607	Sequence 572607,	C 759	10.8	56.8	19	14	US-11-083-784-1425265	Sequence 1425265,
C 687	10.8	56.8	19	14	US-11-083-784-572691	Sequence 572691,	C 760	10.8	56.8	19	14	US-11-083-784-1431142	Sequence 1431142,
C 688	10.8	56.8	19	14	US-11-083-784-580416	Sequence 580416,	C 761	10.8	56.8	19	14	US-11-083-784-1431153	Sequence 1431153,
C 689	10.8	56.8	19	14	US-11-083-784-593993	Sequence 593993,	C 762	10.8	56.8	19	14	US-11-083-784-1443616	Sequence 1443616,
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C 691	10.8	56.8	19	14	US-11-083-784-595682	Sequence 595682,	C 764	10.8	56.8	19	14	US-11-083-784-1456184	Sequence 1456184,
C 692	10.8	56.8	19	14	US-11-083-784-595871	Sequence 595871,	C 765	10.8	56.8	19	14	US-11-083-784-1460761	Sequence 1460761,
C 693	10.8	56.8	19	14	US-11-083-784-599745	Sequence 599745,	C 766	10.8	56.8	19	14	US-11-083-784-1460811	Sequence 1460811,
C 694	10.8	56.8	19	14	US-11-083-784-610550	Sequence 610550,	C 767	10.8	56.8	19	14	US-11-083-784-1460834	Sequence 1460834,
C 695	10.8	56.8	19	14	US-11-083-784-633180	Sequence 633180,	C 768	10.8	56.8	19	14	US-11-083-784-1471448	Sequence 1471448,
C 696	10.8	56.8	19	14	US-11-083-784-646600	Sequence 646600,	C 769	10.8	56.8	19	14	US-11-083-784-1484903	Sequence 1484903,
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C 699	10.8	56.8	19	14	US-11-083-784-658195	Sequence 658195,	C 772	10.8	56.8	19	14	US-11-083-784-1562109	Sequence 1562109,
C 700	10.8	56.8	19	14	US-11-083-784-687518	Sequence 687518,	C 773	10.8	56.8	19	14	US-11-083-784-1589574	Sequence 1589574,
C 701	10.8	56.8	19	14	US-11-083-784-716277	Sequence 716277,	C 774	10.8	56.8	19	15	US-11-101-244-880	Sequence 880, App
C 702	10.8	56.8	19	14	US-11-083-784-716304	Sequence 716304,	C 775	10.8	56.8	19	15	US-11-101-244-1892	Sequence 7892, App
C 703	10.8	56.8	19	14	US-11-083-784-731789	Sequence 731789	C 776	10.8	56.8	19	15	US-11-101-244-15332	Sequence 15392, A
C 704	10.8	56.8	19	14	US-11-083-784-745656	Sequence 745656,	C 777	10.8	56.8	19	15	US-11-101-244-17457	Sequence 17457, A
C 705	10.8	56.8	19	14	US-11-083-784-781918	Sequence 781918,	C 778	10.8	56.8	19	15	US-11-101-244-17554	Sequence 17554, A
C 706	10.8	56.8	19	14	US-11-083-784-788630	Sequence 788630,	C 779	10.8	56.8	19	15	US-11-101-244-17656	Sequence 17656, A
C 707	10.8	56.8	19	14	US-11-083-784-814657	Sequence 814657,	C 780	10.8	56.8	19	15	US-11-101-244-17855	Sequence 17855, A
C 708	10.8	56.8	19	14	US-11-083-784-839928	Sequence 839928,	C 781	10.8	56.8	19	15	US-11-101-244-17965	Sequence 17965, A
C 709	10.8	56.8	19	14	US-11-083-784-873932	Sequence 873932,	C 782	10.8	56.8	19	15	US-11-101-244-17955	Sequence 17955, A
C 710	10.8	56.8	19	14	US-11-083-784-874469	Sequence 874469,	C 783	10.8	56.8	19	15	US-11-101-244-63811	Sequence 63811, A
C 711	10.8	56.8	19	14	US-11-083-784-895717	Sequence 895717,	C 784	10.8	56.8	19	15	US-11-101-244-64010	Sequence 64010, A
C 712	10.8	56.8	19	14	US-11-083-784-909018	Sequence 909018,	C 785	10.8	56.8	19	15	US-11-101-244-640248	Sequence 640248, A
C 713	10.8	56.8	19	14	US-11-083-784-915123	Sequence 915123,	C 786	10.8	56.8	19	15	US-11-101-244-102948	Sequence 102948,
C 714	10.8	56.8	19	14	US-11-083-784-921991	Sequence 921991,	C 787	10.8	56.8	19	15	US-11-101-244-146721	Sequence 146721,
C 715	10.8	56.8	19	14	US-11-083-784-935774	Sequence 935774,	C 788	10.8	56.8	19	15	US-11-101-244-146721	Sequence 146721,
C 716	10.8	56.8	19	14	US-11-083-784-935832	Sequence 935832,	C 789	10.8	56.8	19	15	US-11-101-244-152794	Sequence 152794,
C 717	10.8	56.8	19	14	US-11-083-784-938743	Sequence 938743,	C 790	10.8	56.8	19	15	US-11-101-244-152799	Sequence 152799,
C 718	10.8	56.8	19	14	US-11-083-784-938743	Sequence 938743,	C 791	10.8	56.8	19	15	US-11-101-244-1528127	Sequence 1528127,
C 719	10.8	56.8	19	14	US-11-083-784-949400	Sequence 949400,	C 792	10.8	56.8	19	15	US-11-101-244-162927	Sequence 162927,
C 720	10.8	56.8	19	14	US-11-083-784-949437	Sequence 949437,	C 793	10.8	56.8	19	15	US-11-101-244-165746	Sequence 165746,
C 721	10.8	56.8	19	14	US-11-083-784-963013	Sequence 963013,	C 794	10.8	56.8	19	15	US-11-101-244-196629	Sequence 196629,
C 722	10.8	56.8	19	14	US-11-083-784-986096	Sequence 986096,	C 795	10.8	56.8	19	15	US-11-101-244-196616	Sequence 196616,
C 723	10.8	56.8	19	14	US-11-083-784-992457	Sequence 992457,	C 796	10.8	56.8	19	15	US-11-101-244-202557	Sequence 202557,
C 724	10.8	56.8	19	14	US-11-083-784-1003600	Sequence 1003600,	C 797	10.8	56.8	19	15	US-11-101-244-224249	Sequence 224249,
C 725	10.8	56.8	19	14	US-11-083-784-1003626	Sequence 1003626,	C 798	10.8	56.8	19	15	US-11-101-244-240402	Sequence 240402,
C 726	10.8	56.8	19	14	US-11-083-784-1003658	Sequence 1003658,	C 799	10.8	56.8	19	15	US-11-101-244-240641	Sequence 240641,
C 727	10.8	56.8	19	14	US-11-083-784-1036686	Sequence 1036686,	C 800	10.8	56.8	19	15	US-11-101-244-241175	Sequence 241175,
C 728	10.8	56.8	19	14	US-11-083-784-1041287	Sequence 1041287,	C 801	10.8	56.8	19	15	US-11-101-244-266799	Sequence 266799,
C 729	10.8	56.8	19	14	US-11-083-784-1043478	Sequence 1043478,	C 802	10.8	56.8	19	15	US-11-101-244-266822	Sequence 266822,
C 730	10.8	56.8	19	14	US-11-083-784-1049272	Sequence 1049272,	C 803	10.8	56.8	19	15	US-11-101-244-267407	Sequence 267407,
C 731	10.8	56.8	19	14	US-11-083-784-1051135	Sequence 1051135,	C 804	10.8	56.8	19	15	US-11-101-244-267507	Sequence 267507,
C 732	10.8	56.8	19	14	US-11-083-784-1051181	Sequence 1051181,	C 805	10.8	56.8	19	15	US-11-101-244-267607	Sequence 267607,
C 733	10.8	56.8	19	14	US-11-083-784-1074083	Sequence 1074083,	C 806	10.8	56.8	19	15	US-11-101-244-267707	Sequence 267707,
C 734	10.8	56.8	19	14	US-11-083-784-1084994	Sequence 1084994,	C 807	10.8	56.8	19	15	US-11-101-244-267808	Sequence 267808,
C 735	10.8	56.8	19	14	US-11-083-784-1085100	Sequence 1085100,	C 808	10.8	56.8	19	15	US-11-101-244-273209	Sequence 273209,
C 736	10.8	56.8	19	14	US-11-083-784-1090966	Sequence 1090966,	C 809	10.8	56.8	19	15	US-11-101-244-280504	Sequence 280504,
C 737	10.8	56.8	19	14	US-11-083-784-1113172	Sequence 1113172,	C 810	10.8	56.8	19	15	US-11-101-244-294659	Sequence 294659,
C 738	10.8	56.8	19	14	US-11-083-784-1113250	Sequence 1113250,	C 811	10.8	56.8	19	15	US-11-101-244-324131	Sequence 324131,
C 739	10.8	56.8	19	14	US-11-083-784-1128521	Sequence 1128521,	C 812	10.8	56.8	19	15	US-11-101-244-324232	Sequence 324232,
C 740	10.8	56.8	19	14	US-11-083-784-1143554	Sequence 1143554,	C 813	10.8	56.8	19	15	US-11-101-244-325880	Sequence 325880,
C 741	10.8	56.8	19	14	US-11-083-784-1143583	Sequence 1143583,	C 814	10.8	56.8	19	15	US-11-101-244-325925	Sequence 325925,
C 742	10.8	56.8	19	14	US-11-083-784-1156551	Sequence 1156551,	C 815	10.8	56.8	19	15	US-11-101-244-330918	Sequence 330918,
C 743	10.8	56.8	19	14	US-11-083-784-1156552	Sequence 1156552,	C 816	10.8	56.8	19	15	US-11-101-244-336610	Sequence 336610,
C 744	10.8	56.8	19	14	US-11-083-784-1156552	Sequence 1156552,	C 817	10.8	56.8	19	15	US-11-101-244-336710	Sequence 336710,
C 745	10.8	56.8	19	14	US-11-083-784-1196411	Sequence 1196411,	C 818	10.8	56.8	19	15	US-11-101-244-343306	Sequence 343306,
C 746	10.8	56.8	19	14	US-11-083-784-1196510	Sequence 1196510,	C 819	10.8	56.8	19	15	US-11-101-244-360672	Sequence 360672,
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C 748	10.8	56.8	19	14	US-11-083-784-1277807	Sequence 1277807,							

C 821	10.8	56.8	19	15	US-11-101-244-363791	Sequence 363791,
C 822	10.8	56.8	19	15	US-11-101-244-383845	Sequence 383845,
823	10.8	56.8	19	15	US-11-101-244-389260	Sequence 389260,
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826	10.8	56.8	19	15	US-11-101-244-390712	Sequence 390712,
C 827	10.8	56.8	19	15	US-11-101-244-409751	Sequence 409751,
828	10.8	56.8	19	15	US-11-101-244-434661	Sequence 434661,
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C 836	10.8	56.8	19	15	US-11-101-244-486136	Sequence 486136,
C 837	10.8	56.8	19	15	US-11-101-244-501009	Sequence 501009,
C 838	10.8	56.8	19	15	US-11-101-244-505436	Sequence 505436,
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C 841	10.8	56.8	19	15	US-11-101-244-553705	Sequence 553705,
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C 854	10.8	56.8	19	15	US-11-101-244-599745	Sequence 599745,
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C 866	10.8	56.8	19	15	US-11-101-244-788630	Sequence 788630,
C 867	10.8	56.8	19	15	US-11-101-244-814657	Sequence 814657,
C 868	10.8	56.8	19	15	US-11-101-244-839928	Sequence 839928,
C 869	10.8	56.8	19	15	US-11-101-244-873932	Sequence 873932,
C 870	10.8	56.8	19	15	US-11-101-244-874469	Sequence 874469,
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872	10.8	56.8	19	15	US-11-101-244-909018	Sequence 909018,
C 873	10.8	56.8	19	15	US-11-101-244-915123	Sequence 915123,
C 874	10.8	56.8	19	15	US-11-101-244-921916	Sequence 921916,
C 875	10.8	56.8	19	15	US-11-101-244-921921	Sequence 921921,
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C 877	10.8	56.8	19	15	US-11-101-244-935832	Sequence 935832,
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C 880	10.8	56.8	19	15	US-11-101-244-949437	Sequence 949437,
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C 904	10.8	56.8	19	15	US-11-101-244-1196411	Sequence 1196411,
C 905	10.8	56.8	19	15	US-11-101-244-1196510	Sequence 1196510,
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C 910	10.8	56.8	19	15	US-11-101-244-1281521	Sequence 1281521,
C 911	10.8	56.8	19	15	US-11-101-244-1305609	Sequence 1305609,
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C 941	10.6	55.8	19	10	US-10-863-973-1161	Sequence 938, App
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C 943	10.6	55.8	19	10	US-10-922-675-998	Sequence 938, App
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946	10.6	55.8	19	10	US-10-923-380-108	Sequence 444, App
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C 952	10.6	55.8	19	11	US-10-310-914A-208686	Sequence 208686,
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955	10.6	55.8	19	11	US-10-310-914A-298552	Sequence 298552,
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ALIGNMENTS

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RESULT 1
US-10-636-065-29
; Sequence 29, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens
US-10-636-065-29
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Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CGCAGGATCTCTCTTCA 19
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; Sequence 787223, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 787223
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-787223
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Best Local Similarity 93.8%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 16 CACGGATCTCTCTTCA 1
RESULT 3
US-11-101-244-787223/C
; Sequence 787223, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 787223
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-787223
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Best Local Similarity 93.8%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 3 CACGGATCTCTCTTCA 18
DB 16 CACGGATCTCTCTTCA 1
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Db 16 CACGAGATCTCTCA 1

RESULT 4

US-10-400-382-29

Sequence 29, Application US/10400382

Publication No. US20030190659A1

GENERAL INFORMATION:

APPLICANT: LaCase, Eric

APPLICANT: McManus, Daniel

APPLICANT: Durkin, Jonathan P.

TITLE OF INVENTION: Antisense IAP Nucleobase Oligomers and

TITLE OF INVENTION: Uses Thereof

FILE REFERENCE: 07891/025004

CURRENT APPLICATION NUMBER: US/10/400,382

PRIOR FILING DATE: 2003-03-27

PRIOR APPLICATION NUMBER: US 60/367,853

NUMBER OF SEQ ID NOS: 460

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 29

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: based on Homo sapiens.

OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,

OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog

FEATURE:

NAME/KEY: misc feature

LOCATION: 8, 10, 12, 15, 16

OTHER INFORMATION: n = T or U

US-10-400-382-29

Query Match 73.7%; Score 14; DB 7; Length 19;

Best Local Similarity 73.7%; Pred. No. 3.9e+03;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCTTCAC 19

Db 1 CGCAGCGNANCCNCCAC 19

RESULT 5

US-10-400-382-107

Sequence 107, Application US/10400382

Publication No. US20030190659A1

GENERAL INFORMATION:

APPLICANT: LaCase, Eric

APPLICANT: McManus, Daniel

APPLICANT: Durkin, Jonathan P.

TITLE OF INVENTION: Antisense IAP Nucleobase Oligomers and

TITLE OF INVENTION: Uses Thereof

FILE REFERENCE: 07891/025004

CURRENT APPLICATION NUMBER: US/10/400,382

PRIOR FILING DATE: 2003-03-27

PRIOR APPLICATION NUMBER: US 60/367,853

NUMBER OF SEQ ID NOS: 460

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 107

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: based on Homo sapiens.

OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,

OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog

FEATURE:

NAME/KEY: misc feature

LOCATION: 8, 10, 12, 15, 16

OTHER INFORMATION: n = T or U

US-10-400-382-107

Query Match 73.7%; Score 14; DB 7; Length 19;

Best Local Similarity 73.7%; Pred. No. 3.9e+03;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCTTCAC 19

Db 1 CGCAGCGNANCCNCCAC 19

RESULT 6

US-10-975-790-29

Sequence 29, Application US/10975790

Publication No. US20050119217A1

GENERAL INFORMATION:

APPLICANT: LaCase, Eric

APPLICANT: McManus, Daniel

APPLICANT: Durkin, Jonathan P.

TITLE OF INVENTION: METHODS AND REAGENTS FOR THE TREATMENT

TITLE OF INVENTION: OF PROLIFERATIVE DISEASES

FILE REFERENCE: 07891/039002

CURRENT APPLICATION NUMBER: US/10/975,790

PRIOR FILING DATE: 2004-10-28

PRIOR APPLICATION NUMBER: 60/516,263

NUMBER OF SEQ ID NOS: 490

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 29

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: based on Homo sapiens.

OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,

OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog

FEATURE:

NAME/KEY: misc feature

LOCATION: 8, 10, 12, 15, 16

OTHER INFORMATION: n = T or U

US-10-975-790-29

Query Match 73.7%; Score 14; DB 10; Length 19;

Best Local Similarity 73.7%; Pred. No. 3.9e+03;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCTTCAC 19

Db 1 CGCAGCGNANCCNCCAC 19

RESULT 7

US-10-975-790-107

Sequence 107, Application US/10975790

Publication No. US20050119217A1

GENERAL INFORMATION:

APPLICANT: LaCase, Eric

APPLICANT: McManus, Daniel

APPLICANT: Durkin, Jonathan P.

TITLE OF INVENTION: METHODS AND REAGENTS FOR THE TREATMENT

TITLE OF INVENTION: OF PROLIFERATIVE DISEASES

FILE REFERENCE: 07891/039002

CURRENT APPLICATION NUMBER: US/10/975,790

PRIOR FILING DATE: 2004-10-28

PRIOR APPLICATION NUMBER: 60/516,263

NUMBER OF SEQ ID NOS: 490

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 107

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: based on Homo sapiens.

OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,
OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog
FEATURE:
NAME/KEY: misc feature
LOCATION: 8, 10, 12, 15, 16
OTHER INFORMATION: n = T or U
US-10-975-790-107

Query Match 73.7%; Score 14; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCAGCGATCTCTTCAC 19
DB 1 CGCAGCGANNCNNCACC 19

RESULT 8
US-11-083-784-798689/c
Sequence 798689, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 798689
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-798689

Query Match 70.5%; Score 13.4; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 8.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCTTCAC 19
DB 18 CAGTATCTCTTCAC 4

RESULT 9
US-11-101-244-798689/c
Sequence 798689, Application US/1101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 798689
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-798689

Query Match 70.5%; Score 13.4; DB 15; Length 19;
Best Local Similarity 93.3%; Pred. No. 8.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCTTCAC 19
DB 18 CAGTATCTCTTCAC 4

RESULT 10
US-10-739-904-10/c
Sequence 10, Application US/10739904
Publication No. US20050181373A1
GENERAL INFORMATION:
APPLICANT: SMITH, Timothy P.
APPLICANT: CASAS, Eduardo
TITLE OF INVENTION: Single Nucleotide Polymorphism Markers in the Bovine
FILE REFERENCE: 0103.03 Timothy P. Smith et al.
CURRENT APPLICATION NUMBER: US/10/739,904
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 19
TYPE: DNA
ORGANISM: Bos taurus
US-10-739-904-10

Query Match 68.4%; Score 13; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CACGTATCTCTCT 15
DB 17 CACGTATCTCTCT 5

RESULT 11
US-11-083-784-1156068/c
Sequence 1156068, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1156068
LENGTH: 19
TYPE: RNA


```
; ORGANISM: Homo sapiens
US-11-083-784-1156068

Query Match
Best Local Similarity 68.4%; Score 13; DB 14; Length 19;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTATCTCTCTCA 18
Db 13 GGTATCTCTCTCA 1

RESULT 12
US-11-101-244-1156068/C
; Sequence 1156068, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1156068
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1156068

Query Match
Best Local Similarity 68.4%; Score 13; DB 15; Length 19;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTATCTCTCTCA 18
Db 13 GGTATCTCTCTCA 1

RESULT 13
US-11-083-784-224158/C
; Sequence 224158, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 224158
; LENGTH: 19
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-224158

Query Match
Best Local Similarity 67.4%; Score 12.8; DB 14; Length 19;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCACGGTATCTCTCTC 17
Db 17 GCACGGTATCTCTCTC 2

RESULT 14
US-11-083-784-761475/C
; Sequence 761475, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 761475
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-761475

Query Match
Best Local Similarity 67.4%; Score 12.8; DB 14; Length 19;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCACGGTATCTCTCTC 17
Db 17 GCACGGTATCTCTCTC 2

RESULT 15
US-11-101-244-224158/C
; Sequence 224158, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 224158
```

LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-224158

Query Match 67.4%; Score 12.8; DB 15; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGATATCTCCTTC 17
Db 17 GCACGATATCACCCTC 2

RESULT 16
US-11-101-244-761475/c
Sequence 761475, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 761475
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-761475

Query Match 67.4%; Score 12.8; DB 15; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGATATCTCCTTC 17
Db 17 GCACGATATCCTTC 2

RESULT 17
US-09-969-373-2206
Sequence 2206, Application US/09969373
Patent No. US20020133852A1
GENERAL INFORMATION:
APPLICANT: Eifert, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 2206
LENGTH: 19
TYPE: DNA
ORGANISM: Glycine max
US-09-969-373-2206

Query Match 66.3%; Score 12.6; DB 3; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCTTCAC 19
Db 1 CCACGTCTCTCTTCCTC 19

RESULT 18
US-11-083-784-754/c
Sequence 754, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 754
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-754

Query Match 65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGTATCTCCTT 16
Db 16 CACGGTATCTCCTT 3

RESULT 19
US-11-083-784-183913
Sequence 183913, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 183913
LENGTH: 19

TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-183913

Query Match 65.3% Score 12.4; DB 14; Length 19;
Best Local Similarity 64.3% Pred. No. 2.7e+04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 6 GGATCTCTCTCCAC 19
Db 1 GGAATCCTCCTCCAC 14

RESULT 20

US-11-083-784-222011/c
Sequence 222011, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 222011
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-222011

Query Match 65.3% Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9% Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 CACGATCTCTCTT 16
Db 16 CACGATCTCTCTT 3

RESULT 21

US-11-083-784-475145/c
Sequence 475145, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmoon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary
SEQ ID NO 475145
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-475145

Query Match 65.3% Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9% Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGCAGGATCTCTCC 14
Db 14 CGCAGGATCTCTCC 1

RESULT 22

US-11-083-784-475149/c
Sequence 475149, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmoon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 475149
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-475149

Query Match 65.3% Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9% Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGCAGGATCTCTCC 14
Db 16 CGCAGGATCTCTCC 3

RESULT 23

US-11-083-784-583673/c
Sequence 583673, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmoon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10

;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO: 583673
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-583673

Query Match 65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCTTCA 18
| |||||
Db 14 CAGTATCTCTTCA 1

RESULT 24

US-11-083-784-798632/c
; Sequence 798632, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 798632
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-798632

Query Match 65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCTTCA 18
| |||||
Db 14 CAGTATCTCTTCA 1

RESULT 25

US-11-083-784-873288/c
; Sequence 873288, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333

;; PRIOR FILING DATE: 2003-11-14
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO: 873288
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-873288

Query Match 65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCTTCA 18
| |||||
Db 14 CAGTATCTCTTCA 1

RESULT 26

US-11-083-784-1087813/c
; Sequence 1087813, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1087813
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1087813

Query Match 65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ACGTATCTCTTTC 17
| |||||
Db 18 ACGTATCTCTTTC 5

RESULT 27

US-11-083-784-1087832/c
; Sequence 1087832, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

```

? CURRENT APPLICATION NUMBER: US/11/083,784
? CURRENT FILING DATE: 2005-03-18
? PRIOR APPLICATION NUMBER: US/10/714,333
? PRIOR FILING DATE: 2003-11-14
? PRIOR APPLICATION NUMBER: 60/502,050
? PRIOR FILING DATE: 2003-09-10
? PRIOR APPLICATION NUMBER: 60/426,137
? PRIOR FILING DATE: 2002-11-14
? NUMBER OF SEQ ID NOS: 1591911
? SOFTWARE: Proprietary
? SEQ ID NO 1087832
? LENGTH: 19
? TYPE: RNA
? ORGANISM: Homo sapiens
US-11-083-784-1087832

```

RESULT 28
US-11-083-784-1180480/c
; Sequence 1180480, Application US/11083784
; Publication No. US20050245475A1
Source: ZWISSEN

```

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083, 784
PRIORITY FILING DATE: 2005-03-18
PRIORITY APPLICATION NUMBER: US/10/714, 333
PRIORITY FILING DATE: 2003-11-14
PRIORITY APPLICATION NUMBER: 60/502, 050
PRIORITY FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: 60/426, 137
PRIORITY FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1180480
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-1180480

```

Qy	3	CACGGTATCTCCTT	16
Db	16	CCCGGTATCTCCTT	3

RESULT 29
US-11-083-784-1191739/C
? Sequence 1191739, Application US/11083784
? Publication No. US20050245475A1
? GENERAL INFORMATION:
? APPLICANT: Pharmacom, Inc.
? APPLICANT: Khvorova, Anastasia
? APPLICANT: Reynolds, Angela
? APPLICANT: Leake, Devin
? APPLICANT: Marshall, William

Query Match	65.3%	Score 12.4;	DB 14;	Length 19;
Best Local Similarity	92.9%;	Pred. NO. 2.7e+04;		
Matches 13; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	4	ACGGTATCTCCTTC	17
Db	18	ATGGTATCTCCTTC	5

```

RESULT 30
US-11-083-784-1191772/c
; Sequence 1191772, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Pharmaco, Inc.
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OR INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 114990US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1191772
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1191772

```

Query Match	65.3%	Score 12.4;	DB 14;	Length 19;
Best Local Similarity	92.9%	Pred. No. 2.7e+04;		
Matches 13; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

```

Qy      4  ACGGTATCTCCTTC 17
         | |||||
Db      15  ATGGTATCTCCTTC  2

```

RESULT 31
US-11-083-784/1306236
; Sequence 1306236, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1306236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1306236
```

```

Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 57.1%; Pred. No. 2.7e+04;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 CACGGTATCTCCTTC 16
      ||| | | | | | | | | |
DB      1 CACGUAUUCUCCU 14
```

```

RESULT 32
US-11-083-784-1585329/c
; Sequence 1585329, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1585329
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1585329
```

```

Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
      ||| | | | | | | | | |
DB      18 ACAGTATCTCCTTC 5
```

```

RESULT 33
US-11-083-784-1585348/c
; Sequence 1585348, Application US/11083784
; Publication No. US20050245475A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1585348
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1585348
```

```

Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
      ||| | | | | | | | | |
DB      15 ACAGTATCTCCTTC 2
```

```

RESULT 34
US-11-101-244-754/c
; Sequence 754, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 754
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-754
```

```

Query Match      65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 CACGGTATCTCCTTC 16
      ||| | | | | | | | | |
DB      16 CACGGTATCTCCTTC 3
```

```

RESULT 35
US-11-101-244-183913
; Sequence 183913, Application US/1101244
```

Fri Aug 11 11:55:57 2006

```

; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 183913
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-183913

```

```

Query Match      65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 64.3%; Pred. No. 2.7e+04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      6 GGTATCTCTCTTCAC 19
Db      1 GGAUUCUCUCUCCAC 14

RESULT 36
US-11-101-244-222011/c
; Sequence 222011, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 222011
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-222011

```

```

Query Match      65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      3 CACGGTATCTCTTC 16
Db      16 CACGGTATCTCTTC 3

RESULT 37
US-11-101-244-475145/c
; Sequence 475145, Application US/11101244
; Publication No. US20050246794A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 475145
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-475145

```

```

Query Match      65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      1 CGCACGGTATCTTCC 14
Db      14 CGCACGGTATCTTCC 1

RESULT 38
US-11-101-244-475149/c
; Sequence 475149, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 475149
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-475149

```

```

Query Match      65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      1 CGCACGGTATCTTCC 14
Db      16 CGCACGGTATCTTCC 3

RESULT 39
US-11-101-244-583673/c
; Sequence 583673, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 583673
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-583673

```

```

Query Match          65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      5 CGGTATCTCCTTCA 18
      | |||||
Db      14 CAGTATCTCCTTCA 1

```

```

RESULT 40
US-11-101-244-798632/c
; Sequence 798632, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 798632
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-798632

```

```

Query Match          65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      5 CGGTATCTCCTTCA 18
      | |||||
Db      14 CAGTATCTCCTTCA 1

```

Search completed: August 10, 2006, 09:22:26
 Job time : 641.333 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using bw model

Run on: August 10, 2006, 08:51:05 ; Search time 88.3333 Seconds
(without alignments)
341.586 Million cell updates/sec

Title: US-10-636-065-29
Perfect score: 19
Sequence: 1 cgcacgctactcttcac 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 27232

Minimum DB seq length: 19
Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications NA New:*
1: /EMC_Celerra_SIDS3/prodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/prodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/prodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/prodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/prodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/prodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	57.9	19	US-10-921-554-39	Sequence 39, App1
2	11	57.9	19	US-10-921-554-139	Sequence 139, App
3	10.6	55.8	19	US-11-293-697-5004	Sequence 5004, App
4	10	52.6	19	US-11-217-936-416	Sequence 416, App
5	10	52.6	19	US-11-217-936-526	Sequence 526, App
6	10	52.6	19	US-11-217-936-1455	Sequence 1455, App
7	10	52.6	19	US-11-217-936-1924	Sequence 1924, App
8	9.8	51.6	19	US-10-921-554-94	Sequence 94, App1
9	9.8	51.6	19	US-10-921-554-194	Sequence 194, App
10	9.8	51.6	19	US-11-344-702-269	Sequence 269, App
11	9.8	51.6	19	US-11-344-702-270	Sequence 270, App
12	9.8	51.6	19	US-11-344-702-271	Sequence 271, App
13	9.8	51.6	19	US-11-345-361-269	Sequence 269, App
14	9.8	51.6	19	US-11-345-361-270	Sequence 270, App
15	9.8	51.6	19	US-11-345-361-271	Sequence 271, App
16	9.8	51.6	19	US-11-217-936-98	Sequence 98, App1
17	9.8	51.6	19	US-11-217-936-213	Sequence 213, App
18	9.8	51.6	19	US-11-217-936-2810	Sequence 2810, App
19	9.8	51.6	19	US-11-217-936-3037	Sequence 3037, App
20	9.6	50.5	19	US-10-424-339-335	Sequence 335, App
21	9.6	50.5	19	US-10-424-339-440	Sequence 440, App
22	9.6	50.5	19	US-11-102-097-517	Sequence 517, App
23	9.4	49.5	19	US-11-256-694-308	Sequence 308, App

24	9.4	49.5	19	US-11-256-694-319	Sequence 319, App
25	9.4	49.5	19	US-11-256-694-332	Sequence 332, App
26	9.4	49.5	19	US-11-256-694-333	Sequence 333, App
27	9.4	49.5	19	US-11-256-694-340	Sequence 340, App
28	9.4	49.5	19	US-11-256-694-351	Sequence 351, App
29	9.4	49.5	19	US-11-256-694-362	Sequence 362, App
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C 267	7.8	41.1	19	9	US-11-217-936-433	Sequence 433, App	C 340	7.6	40.0	19	9	US-11-217-936-2381	Sequence 2381, App
C 268	7.8	41.1	19	9	US-11-217-936-543	Sequence 543, App	C 341	7.6	40.0	19	9	US-11-217-936-2779	Sequence 2779, App
C 269	7.8	41.1	19	9	US-11-217-936-1043	Sequence 1043, App	C 342	7.6	40.0	19	9	US-11-217-936-2885	Sequence 2885, App
C 270	7.8	41.1	19	9	US-11-217-936-1066	Sequence 1066, App	C 343	7.6	40.0	19	9	US-11-217-936-2961	Sequence 2961, App
C 271	7.8	41.1	19	9	US-11-217-936-1180	Sequence 1180, App	C 344	7.6	40.0	19	9	US-11-217-936-3006	Sequence 3006, App
C 272	7.8	41.1	19	9	US-11-217-936-1284	Sequence 1284, App	C 345	7.6	40.0	19	9	US-11-217-936-3112	Sequence 3112, App
273	7.8	41.1	19	9	US-11-217-936-1512	Sequence 1512, App	C 346	7.6	40.0	19	9	US-11-217-936-3188	Sequence 3188, App
274	7.8	41.1	19	9	US-11-217-936-1535	Sequence 1535, App	C 347	7.6	40.0	19	9	US-11-217-936-3449	Sequence 3449, App
275	7.8	41.1	19	9	US-11-217-936-1649	Sequence 1649, App	C 348	7.6	40.0	19	9	US-11-217-936-3475	Sequence 3475, App
C 276	7.8	41.1	19	9	US-11-217-936-1753	Sequence 1753, App	C 349	7.6	40.0	19	9	US-11-217-936-3623	Sequence 3623, App
C 277	7.8	41.1	19	9	US-11-217-936-2203	Sequence 2203, App	C 350	7.6	40.0	19	9	US-11-217-936-3648	Sequence 3648, App
C 278	7.8	41.1	19	9	US-11-217-936-2498	Sequence 2498, App	C 351	7.6	40.0	19	9	US-11-217-936-3826	Sequence 3826, App
C 279	7.8	41.1	19	9	US-11-217-936-4390	Sequence 4390, App	C 352	7.6	40.0	19	9	US-11-217-936-3922	Sequence 3922, App
C 280	7.8	41.1	19	9	US-11-217-936-4683	Sequence 4683, App	C 353	7.6	40.0	19	9	US-11-217-936-4030	Sequence 4030, App
C 281	7.8	41.1	19	9	US-11-217-936-4413	Sequence 4413, App	C 354	7.6	40.0	19	9	US-11-217-936-4030	Sequence 4030, App
C 282	7.8	41.1	19	9	US-11-217-936-4414	Sequence 4414, App	C 355	7.6	40.0	19	9	US-11-217-936-4030	Sequence 4030, App
C 283	7.8	41.1	19	9	US-11-217-936-4714	Sequence 4714, App	C 356	7.6	40.0	19	9	US-11-217-936-4714	Sequence 4714, App
284	7.8	41.1	19	9	US-11-217-936-4811	Sequence 4811, App	C 357	7.6	40.0	19	9	US-11-217-936-4811	Sequence 4811, App
285	7.8	41.1	19	9	US-11-233-495-24	Sequence 24, App1	C 358	7.6	40.0	19	9	US-11-217-936-4811	Sequence 4811, App
C 286	7.8	41.1	19	9	US-11-102-097-1099	Sequence 1099, App	C 359	7.6	40.0	19	9	US-11-102-097-1402	Sequence 1402, App
C 287	7.8	41.1	19	9	US-11-102-097-1100	Sequence 1100, App	C 360	7.6	40.0	19	9	US-11-102-097-1402	Sequence 1402, App
C 288	7.8	41.1	19	9	US-11-102-097-1101	Sequence 1101, App	C 361	7.6	40.0	19	9	US-11-102-097-1402	Sequence 1402, App
C 289	7.8	41.1	19	9	US-11-102-097-1270	Sequence 1270, App	C 362	7.6	40.0	19	9	US-11-102-097-1402	Sequence 1402, App
C 290	7.8	41.1	19	9	US-11-102-097-1558	Sequence 1558, App	C 363	7.6	40.0	19	9	US-11-267-769-24	Sequence 24, App1
C 291	7.8	41.1	19	9	US-11-102-097-1559	Sequence 1559, App	C 364	7.6	40.0	19	9	US-11-267-769-24	Sequence 24, App1
C 292	7.8	41.1	19	9	US-11-102-097-1560	Sequence 1560, App	C 365	7.6	40.0	19	9	US-11-267-769-24	Sequence 24, App1
C 293	7.8	41.1	19	9	US-11-102-097-1989	Sequence 1989, App	C 366	7.6	40.0	19	9	US-11-267-769-24	Sequence 24, App1
C 294	7.8	41.1	19	9	US-11-102-097-2079	Sequence 2079, App	C 367	7.6	40.0	19	9	US-11-267-769-24	Sequence 24, App1
C 295	7.8	41.1	19	9	US-11-102-097-2080	Sequence 2080, App	C 368	7.6	40.0	19	9	US-11-267-769-24	Sequence 24, App1
296	7.8	41.1	19	9	US-11-501-814-11	Sequence 11, App1	C 369	7.6	40.0	19	9	US-11-267-769-24	Sequence 24, App1
297	7.6	40.0	19	6	US-10-514-776-6	Sequence 6, App1	C 370	7.4	38.9	19	6	US-10-424-339-126	Sequence 126, App
298	7.6	40.0	19	6	US-10-514-776-203	Sequence 203, App	C 371	7.4	38.9	19	6	US-10-424-339-227	Sequence 227, App
299	7.6	40.0	19	6	US-10-515-598-11	Sequence 11, App1	C 372	7.4	38.9	19	6	US-10-424-339-289	Sequence 289, App
C 300	7.6	40.0	19	6	US-10-469-938A-68	Sequence 68, App	C 373	7.4	38.9	19	6	US-10-424-339-404	Sequence 404, App
C 301	7.6	40.0	19	6	US-10-469-938A-1513	Sequence 1513, App	C 374	7.4	38.9	19	6	US-10-424-339-509	Sequence 509, App
C 302	7.6	40.0	19	6	US-10-424-339-58	Sequence 58, App1	C 375	7.4	38.9	19	6	US-10-424-339-592	Sequence 592, App
C 303	7.6	40.0	19	6	US-10-424-339-80	Sequence 80, App1	C 376	7.4	38.9	19	6	US-10-424-339-600	Sequence 600, App
C 304	7.6	40.0	19	6	US-10-424-339-221	Sequence 221, App	C 377	7.4	38.9	19	6	US-10-424-339-679	Sequence 679, App
C 305	7.6	40.0	19	6	US-10-424-339-243	Sequence 243, App	C 378	7.4	38.9	19	6	US-10-424-339-699	Sequence 699, App
C 306	7.6	40.0	19	6	US-10-424-339-391	Sequence 391, App	C 379	7.4	38.9	19	6	US-10-424-339-723	Sequence 723, App
C 307	7.6	40.0	19	6	US-10-424-339-496	Sequence 496, App	C 380	7.4	38.9	19	6	US-10-424-339-809	Sequence 809, App
C 308	7.6	40.0	19	6	US-10-424-339-711	Sequence 711, App	C 381	7.4	38.9	19	6	US-10-424-339-820	Sequence 820, App
C 309	7.6	40.0	19	6	US-10-424-339-920	Sequence 920, App	C 382	7.4	38.9	19	6	US-10-424-339-861	Sequence 861, App
C 310	7.6	40.0	19	6	US-10-424-339-1421	Sequence 1421, App	C 383	7.4	38.9	19	6	US-10-424-339-908	Sequence 908, App
C 311	7.6	40.0	19	6	US-10-424-339-1602	Sequence 1602, App	C 384	7.4	38.9	19	6	US-10-424-339-932	Sequence 932, App
C 312	7.6	40.0	19	6	US-10-997-086-88	Sequence 88, App1	C 385	7.4	38.9	19	6	US-10-424-339-1018	Sequence 1018, App
C 313	7.6	40.0	19	6	US-10-525-726-14	Sequence 14, App1	C 386	7.4	38.9	19	6	US-10-424-339-1029	Sequence 1029, App
C 314	7.6	40.0	19	6	US-10-536-932-54	Sequence 54, App1	C 387	7.4	38.9	19	6	US-10-424-339-1070	Sequence 1070, App
C 315	7.6	40.0	19	6	US-10-525-273-29	Sequence 29, App1	C 388	7.4	38.9	19	6	US-10-424-339-1340	Sequence 1340, App

389	7.4	38.9	19	6	US-10-424-339-1521	Sequence 1521, Ap	C 462	7.4	38.9	19	9	US-11-217-936-3607	Sequence 3607, Ap
C 390	7.4	38.9	19	6	US-10-921-554-12	Sequence 12, Appl	C 463	7.4	38.9	19	9	US-11-217-936-3818	Sequence 3818, Ap
391	7.4	38.9	19	6	US-10-921-554-112	Sequence 112, Appl	C 464	7.4	38.9	19	9	US-11-217-936-3844	Sequence 3844, Ap
392	7.4	38.9	19	6	US-10-536-932-88	Sequence 88, Appl	C 465	7.4	38.9	19	9	US-11-217-936-3850	Sequence 3850, Ap
393	7.4	38.9	19	6	US-10-534-864-20	Sequence 20, Appl	C 466	7.4	38.9	19	9	US-11-217-936-3856	Sequence 3856, Ap
C 394	7.4	38.9	19	6	US-10-825-485-163	Sequence 163, Appl	C 467	7.4	38.9	19	9	US-11-217-936-3866	Sequence 3866, Ap
C 395	7.4	38.9	19	6	US-10-825-485-270	Sequence 270, App	C 468	7.4	38.9	19	9	US-11-217-936-3914	Sequence 3914, Ap
C 396	7.4	38.9	19	6	US-10-825-485-470	Sequence 470, App	C 469	7.4	38.9	19	9	US-11-217-936-3940	Sequence 3940, Ap
397	7.4	38.9	19	6	US-10-825-485-577	Sequence 577, App	C 470	7.4	38.9	19	9	US-11-217-936-3946	Sequence 3946, Ap
398	7.4	38.9	19	7	US-11-817-120-2	Sequence 2, Appl1	C 471	7.4	38.9	19	9	US-11-217-936-3952	Sequence 3952, Ap
399	7.4	38.9	19	7	US-11-813-210-31	Sequence 31, Appl1	C 472	7.4	38.9	19	9	US-11-217-936-3962	Sequence 3962, Ap
C 400	7.4	38.9	19	7	US-11-313-210-60	Sequence 60, Appl	C 473	7.4	38.9	19	9	US-11-217-936-4091	Sequence 4091, Ap
401	7.4	38.9	19	7	US-11-344-702-109	Sequence 109, Appl	C 474	7.4	38.9	19	9	US-11-217-936-4160	Sequence 4160, Ap
402	7.4	38.9	19	7	US-11-344-702-114	Sequence 114, Appl	C 475	7.4	38.9	19	9	US-11-217-936-4242	Sequence 4242, Ap
C 403	7.4	38.9	19	7	US-11-344-702-334	Sequence 334, Appl	C 476	7.4	38.9	19	9	US-11-217-936-4263	Sequence 4263, Ap
C 404	7.4	38.9	19	7	US-11-344-702-349	Sequence 349, Appl	C 477	7.4	38.9	19	9	US-11-217-936-4303	Sequence 4303, Ap
C 405	7.4	38.9	19	7	US-11-344-702-419	Sequence 419, Appl	C 478	7.4	38.9	19	9	US-11-217-936-4349	Sequence 4349, Ap
C 406	7.4	38.9	19	7	US-11-344-702-541	Sequence 541, Appl	C 479	7.4	38.9	19	9	US-11-217-936-4418	Sequence 4418, Ap
C 407	7.4	38.9	19	7	US-11-344-702-542	Sequence 542, Appl	C 480	7.4	38.9	19	9	US-11-217-936-4500	Sequence 4500, Ap
408	7.4	38.9	19	7	US-11-344-702-631	Sequence 631, Appl	C 481	7.4	38.9	19	9	US-11-217-936-4521	Sequence 4521, Ap
409	7.4	38.9	19	7	US-11-344-702-632	Sequence 632, Appl	C 482	7.4	38.9	19	9	US-11-217-936-4561	Sequence 4561, Ap
C 410	7.4	38.9	19	7	US-11-344-702-634	Sequence 634, Appl	C 483	7.4	38.9	19	9	US-11-182-336-54	Sequence 54, Appl
C 411	7.4	38.9	19	7	US-11-345-361-109	Sequence 109, Appl	C 484	7.4	38.9	19	9	US-11-102-097-274	Sequence 274, Appl
412	7.4	38.9	19	7	US-11-345-361-114	Sequence 114, Appl	C 485	7.4	38.9	19	9	US-11-102-097-346	Sequence 346, Appl
C 413	7.4	38.9	19	7	US-11-345-361-334	Sequence 334, Appl	C 486	7.4	38.9	19	9	US-11-102-097-347	Sequence 347, Appl
C 414	7.4	38.9	19	7	US-11-345-361-334	Sequence 334, Appl	C 487	7.4	38.9	19	9	US-11-102-097-348	Sequence 348, Appl
C 415	7.4	38.9	19	7	US-11-345-361-349	Sequence 349, Appl	C 488	7.4	38.9	19	9	US-11-102-097-375	Sequence 375, Appl
C 416	7.4	38.9	19	7	US-11-345-361-541	Sequence 541, Appl	C 489	7.4	38.9	19	9	US-11-102-097-376	Sequence 376, Appl
C 417	7.4	38.9	19	7	US-11-345-361-542	Sequence 542, Appl	C 490	7.4	38.9	19	9	US-11-102-097-377	Sequence 377, Appl
418	7.4	38.9	19	7	US-11-345-361-631	Sequence 631, Appl	C 491	7.4	38.9	19	9	US-11-102-097-378	Sequence 378, Appl
C 419	7.4	38.9	19	7	US-11-345-361-632	Sequence 632, Appl	C 492	7.4	38.9	19	9	US-11-102-097-475	Sequence 475, Appl
C 420	7.4	38.9	19	8	US-11-251-465-131	Sequence 131, Appl	C 493	7.4	38.9	19	9	US-11-102-097-476	Sequence 476, Appl
C 421	7.4	38.9	19	8	US-11-251-465-151	Sequence 151, Appl	C 494	7.4	38.9	19	9	US-11-102-097-477	Sequence 477, Appl
C 422	7.4	38.9	19	8	US-11-251-465-193	Sequence 193, Appl	C 495	7.4	38.9	19	9	US-11-102-097-478	Sequence 478, Appl
C 423	7.4	38.9	19	8	US-11-251-465-407	Sequence 407, Appl	C 496	7.4	38.9	19	9	US-11-102-097-960	Sequence 960, Appl
C 424	7.4	38.9	19	8	US-11-251-465-777	Sequence 777, Appl	C 497	7.4	38.9	19	9	US-11-102-097-961	Sequence 961, Appl
C 425	7.4	38.9	19	8	US-11-251-465-829	Sequence 829, Appl	C 498	7.4	38.9	19	9	US-11-102-097-11025	Sequence 11025, Ap
426	7.4	38.9	19	8	US-11-267-182-11	Sequence 11, Appl	C 500	7.4	38.9	19	9	US-11-102-097-1148	Sequence 1148, Ap
427	7.4	38.9	19	8	US-11-233-507-31	Sequence 31, Appl	C 501	7.4	38.9	19	9	US-11-102-097-11228	Sequence 1149, Ap
428	7.4	38.9	19	8	US-11-293-697-546	Sequence 546, Ap	C 502	7.4	38.9	19	9	US-11-102-097-1224	Sequence 1224, Ap
C 429	7.4	38.9	19	8	US-11-222-565-54	Sequence 54, Appl	C 503	7.4	38.9	19	9	US-11-102-097-1234	Sequence 1234, Ap
C 430	7.4	38.9	19	9	US-11-217-936-58	Sequence 58, Appl	C 504	7.4	38.9	19	9	US-11-102-097-1396	Sequence 1396, Ap
C 431	7.4	38.9	19	9	US-11-217-936-83	Sequence 83, Appl	C 505	7.4	38.9	19	9	US-11-102-097-1397	Sequence 1473, Ap
C 432	7.4	38.9	19	9	US-11-217-936-173	Sequence 173, Appl	C 506	7.4	38.9	19	9	US-11-102-097-1474	Sequence 1474, Ap
433	7.4	38.9	19	9	US-11-217-936-178	Sequence 178, Appl	C 507	7.4	38.9	19	9	US-11-102-097-1475	Sequence 1475, Ap
C 434	7.4	38.9	19	9	US-11-217-936-395	Sequence 395, Appl	C 508	7.4	38.9	19	9	US-11-102-097-1476	Sequence 1476, Ap
C 435	7.4	38.9	19	9	US-11-217-936-505	Sequence 505, Appl	C 509	7.4	38.9	19	9	US-11-102-097-1477	Sequence 1477, Ap
436	7.4	38.9	19	9	US-11-217-936-684	Sequence 684, Appl	C 510	7.4	38.9	19	9	US-11-102-097-1950	Sequence 1950, Ap
C 437	7.4	38.9	19	9	US-11-217-936-761	Sequence 761, Appl	C 511	7.4	38.9	19	9	US-11-102-097-2138	Sequence 2138, Ap
C 438	7.4	38.9	19	9	US-11-217-936-792	Sequence 792, Appl	C 512	7.4	38.9	19	9	US-11-102-097-2139	Sequence 2139, Ap
C 439	7.4	38.9	19	9	US-11-217-936-869	Sequence 869, Appl	C 513	7.4	38.9	19	9	US-11-102-097-2140	Sequence 2140, Ap
440	7.4	38.9	19	9	US-11-217-936-1202	Sequence 1202, Ap	C 514	7.4	38.9	19	9	US-11-102-097-2141	Sequence 2141, Ap
C 441	7.4	38.9	19	9	US-11-217-936-1331	Sequence 1331, Appl	C 515	7.4	38.9	19	9	US-11-102-097-2712	Sequence 2712, Ap
442	7.4	38.9	19	9	US-11-217-936-1360	Sequence 1360, Appl	C 516	7.4	38.9	19	9	US-11-102-097-2840	Sequence 2840, Ap
C 443	7.4	38.9	19	9	US-11-217-936-1671	Sequence 1671, Appl	C 517	7.4	38.9	19	9	US-11-102-097-2881	Sequence 2881, Ap
444	7.4	38.9	19	9	US-11-217-936-1800	Sequence 1800, Appl	C 518	7.4	38.9	19	9	US-11-267-769-14	Sequence 14, Appl
C 445	7.4	38.9	19	9	US-11-217-936-2246	Sequence 2246, Appl	C 519	7.4	38.9	19	9	US-11-267-807-14	Sequence 14, Appl
C 446	7.4	38.9	19	9	US-11-217-936-22502	Sequence 22502, Appl	C 520	7.4	38.9	19	9	US-10-501-834-192	Sequence 182, Appl
447	7.4	38.9	19	9	US-11-217-936-2251	Sequence 2251, Appl	C 521	7.2	37.9	19	6	US-10-501-834-189	Sequence 2041, Ap
C 448	7.4	38.9	19	9	US-11-217-936-2207	Sequence 2207, Appl	C 522	7.2	37.9	19	6	US-10-511-937-70	Sequence 70, Appl
C 449	7.4	38.9	19	9	US-11-217-936-2223	Sequence 2223, Appl	C 523	7.2	37.9	19	6	US-10-514-776-121	Sequence 121, Appl
C 450	7.4	38.9	19	9	US-11-217-936-2296	Sequence 2296, Appl	C 524	7.2	37.9	19	6	US-10-514-776-141	Sequence 141, Appl
C 451	7.4	38.9	19	9	US-11-217-936-2446	Sequence 2446, Appl	C 525	7.2	37.9	19	6	US-10-514-776-142	Sequence 142, Appl
452	7.4	38.9	19	9	US-11-217-936-2502	Sequence 2502, Appl	C 526	7.2	37.9	19	6	US-10-424-339-177	Sequence 277, Appl
453	7.4	38.9	19	9	US-11-217-936-2518	Sequence 2518, Appl	C 527	7.2	37.9	19	6	US-10-424-339-560	Sequence 560, Appl
454	7.4	38.9	19	9	US-11-217-936-2551	Sequence 2551, Appl	C 528	7.2	37.9	19	6	US-10-424-339-639	Sequence 639, Appl
C 455	7.4	38.9	19	9	US-11-217-936-2794	Sequence 2794, Appl	C 529	7.2	37.9	19	6	US-10-424-339-700	Sequence 700, Appl
C 456	7.4	38.9	19	9	US-11-217-936-3021	Sequence 3021, Appl	C 530	7.2	37.9	19	6	US-10-424-339-762	Sequence 762, Appl
C 457	7.4	38.9	19	9	US-11-217-936-3365	Sequence 3365, Appl	C 531	7.2	37.9	19	6	US-10-424-339-850	Sequence 850, Appl
C 458	7.4	38.9	19	9	US-11-217-936-3393	Sequence 3393, Appl	C 532	7.2	37.9	19	6		
C 459	7.4	38.9	19	9	US-11-217-936-3434	Sequence 3434, Appl	C 533	7.2	37.9	19	6		
C 460	7.4	38.9	19	9	US-11-217-936-3538	Sequence 3538, Appl	C 534	7.2	37.9	19	6		
461	7.4	38.9	19	9	US-11-217-936-3566	Sequence 3566, Appl							

535	7.2	37.9	19	6	US-10-424-339-909	Sequence 909, App	C 608	7.2	37.9	19	9	US-11-102-097-398	Sequence 398, App
536	7.2	37.9	19	6	US-10-424-339-971	Sequence 971, App	C 609	7.2	37.9	19	9	US-11-102-097-500	Sequence 500, App
C 537	7.2	37.9	19	6	US-10-424-339-1059	Sequence 1059, App	C 610	7.2	37.9	19	9	US-11-102-097-501	Sequence 501, App
C 538	7.2	37.9	19	6	US-10-424-339-1259	Sequence 1259, App	C 611	7.2	37.9	19	9	US-11-102-097-624	Sequence 624, App
539	7.2	37.9	19	6	US-10-424-339-1324	Sequence 1324, App	C 612	7.2	37.9	19	9	US-11-102-097-625	Sequence 625, App
540	7.2	37.9	19	6	US-10-424-339-1440	Sequence 1440, App	C 613	7.2	37.9	19	9	US-11-102-097-626	Sequence 626, App
C 541	7.2	37.9	19	6	US-10-424-339-1505	Sequence 1505, App	C 614	7.2	37.9	19	9	US-11-102-097-677	Sequence 677, App
542	7.2	37.9	19	6	US-10-881-580-126	Sequence 126, App	C 615	7.2	37.9	19	9	US-11-102-097-1305	Sequence 1305, App
C 543	7.2	37.9	19	6	US-10-881-580-254	Sequence 254, App	C 616	7.2	37.9	19	9	US-11-102-097-1306	Sequence 1306, App
C 544	7.2	37.9	19	6	US-10-921-554-68	Sequence 68, App	C 617	7.2	37.9	19	9	US-11-102-097-1307	Sequence 1307, App
545	7.2	37.9	19	6	US-10-921-554-89	Sequence 89, App	C 618	7.2	37.9	19	9	US-11-102-097-1308	Sequence 1308, App
546	7.2	37.9	19	6	US-10-921-554-169	Sequence 169, App	C 619	7.2	37.9	19	9	US-11-102-097-1309	Sequence 1309, App
C 547	7.2	37.9	19	6	US-10-921-554-188	Sequence 188, App	C 620	7.2	37.9	19	9	US-11-102-097-1399	Sequence 1399, App
548	7.2	37.9	19	6	US-10-516-314-6	Sequence 6, App	C 621	7.2	37.9	19	9	US-11-102-097-1400	Sequence 1400, App
C 549	7.2	37.9	19	6	US-10-514-558-35	Sequence 35, App	C 622	7.2	37.9	19	9	US-11-102-097-1535	Sequence 1535, App
550	7.2	37.9	19	7	US-11-299-025-124	Sequence 124, App	C 623	7.2	37.9	19	9	US-11-102-097-1536	Sequence 1536, App
C 551	7.2	37.9	19	7	US-11-344-702-356	Sequence 356, App	C 624	7.2	37.9	19	9	US-11-102-097-1657	Sequence 1657, App
C 552	7.2	37.9	19	7	US-11-344-702-418	Sequence 418, App	C 625	7.2	37.9	19	9	US-11-102-097-1658	Sequence 1658, App
C 553	7.2	37.9	19	7	US-11-344-702-433	Sequence 433, App	C 626	7.2	37.9	19	9	US-11-102-097-1686	Sequence 1686, App
C 554	7.2	37.9	19	7	US-11-344-702-547	Sequence 547, App	C 627	7.2	37.9	19	9	US-11-102-097-1687	Sequence 1687, App
C 555	7.2	37.9	19	7	US-11-345-361-356	Sequence 356, App	C 628	7.2	37.9	19	9	US-11-102-097-1688	Sequence 1688, App
C 556	7.2	37.9	19	7	US-11-345-361-418	Sequence 418, App	C 629	7.2	37.9	19	9	US-11-102-097-1689	Sequence 1689, App
C 557	7.2	37.9	19	7	US-11-345-361-433	Sequence 433, App	C 630	7.2	37.9	19	9	US-11-102-097-1745	Sequence 1745, App
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559	7.2	37.9	19	8	US-11-251-465-485	Sequence 485, App	C 632	7.2	37.9	19	9	US-11-102-097-1747	Sequence 1747, App
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561	7.2	37.9	19	8	US-11-251-465-759	Sequence 759, App	C 634	7.2	37.9	19	9	US-11-102-097-1956	Sequence 1956, App
C 562	7.2	37.9	19	8	US-11-293-697-5208	Sequence 5208, App	C 635	7.2	37.9	19	9	US-11-102-097-2051	Sequence 2051, App
C 563	7.2	37.9	19	8	US-11-321-421-278	Sequence 278, App	C 636	7.2	37.9	19	9	US-11-102-097-2052	Sequence 2052, App
564	7.2	37.9	19	8	US-11-321-991-7	Sequence 7, App	C 637	7.2	37.9	19	9	US-11-102-097-2053	Sequence 2053, App
C 565	7.2	37.9	19	9	US-11-217-936-56	Sequence 56, App	C 638	7.2	37.9	19	9	US-11-102-097-2054	Sequence 2054, App
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567	7.2	37.9	19	9	US-11-217-936-171	Sequence 171, App	C 640	7.2	37.9	19	9	US-11-102-097-2463	Sequence 2463, App
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C 576	7.2	37.9	19	9	US-11-217-936-1927	Sequence 1927, App	C 649	7.2	37.9	19	6	US-10-987-453-144	Sequence 144, App
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C 579	7.2	37.9	19	9	US-11-217-936-2506	Sequence 2506, App	C 652	7.2	37.9	19	6	US-10-525-360-7	Sequence 7, App
C 580	7.2	37.9	19	9	US-11-217-936-2599	Sequence 2599, App	C 653	7.2	37.9	19	6	US-10-540-460-116	Sequence 116, App
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582	7.2	37.9	19	9	US-11-217-936-2863	Sequence 2863, App	C 655	7.2	37.9	19	6	US-10-424-339-169	Sequence 169, App
583	7.2	37.9	19	9	US-11-217-936-2958	Sequence 2958, App	C 656	7.2	37.9	19	6	US-10-424-339-387	Sequence 387, App
584	7.2	37.9	19	9	US-11-217-936-2995	Sequence 2995, App	C 657	7.2	37.9	19	6	US-10-424-339-420	Sequence 420, App
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C 588	7.2	37.9	19	9	US-11-217-936-3439	Sequence 3439, App	C 661	7.2	37.9	19	6	US-10-424-339-582	Sequence 582, App
589	7.2	37.9	19	9	US-11-217-936-3612	Sequence 3612, App	C 662	7.2	37.9	19	6	US-10-424-339-617	Sequence 617, App
C 590	7.2	37.9	19	9	US-11-217-936-3833	Sequence 3833, App	C 663	7.2	37.9	19	6	US-10-424-339-661	Sequence 661, App
C 591	7.2	37.9	19	9	US-11-217-936-3929	Sequence 3929, App	C 664	7.2	37.9	19	6	US-10-424-339-756	Sequence 756, App
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594	7.2	37.9	19	9	US-11-217-936-4411	Sequence 4411, App	C 667	7.2	37.9	19	6	US-10-424-339-965	Sequence 965, App
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C 596	7.2	37.9	19	9	US-11-217-936-4798	Sequence 4798, App	C 669	7.2	37.9	19	6	US-10-424-339-1104	Sequence 1104, App
C 597	7.2	37.9	19	9	US-11-217-936-4895	Sequence 4895, App	C 670	7.2	37.9	19	6	US-10-536-804-25	Sequence 25, App
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C 601	7.2	37.9	19	9	US-11-267-381-34	Sequence 34, App	C 674	7.2	37.9	19	6	US-10-881-580-17	Sequence 17, App
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C 607	7.2	37.9	19	9	US-11-102-097-397	Sequence 397, App	C 680	7.2	37.9	19	6	US-10-825-485-99	Sequence 99, App

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C 682	7	36.8	19	6	US-10-825-485-124	Sequence 124, App	C 755	7	36.8	19	9	US-11-217-936-2246	Sequence 2246, Ap
C 683	7	36.8	19	6	US-10-825-485-207	Sequence 207, App	C 756	7	36.8	19	9	US-11-217-936-2289	Sequence 2289, Ap
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C 685	7	36.8	19	6	US-10-825-485-406	Sequence 406, App	C 758	7	36.8	19	9	US-11-217-936-2394	Sequence 2394, Ap
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C 687	7	36.8	19	6	US-10-825-485-431	Sequence 431, App	C 760	7	36.8	19	9	US-11-217-936-2541	Sequence 2541, Ap
C 688	7	36.8	19	6	US-10-825-485-514	Sequence 514, App	C 761	7	36.8	19	9	US-11-217-936-2584	Sequence 2584, Ap
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C 692	7	36.8	19	6	US-10-479-225A-271	Sequence 271, App	C 765	7	36.8	19	9	US-11-217-936-2868	Sequence 2868, Ap
C 693	7	36.8	19	7	US-11-399-025-45	Sequence 45, App1	C 766	7	36.8	19	9	US-11-217-936-3018	Sequence 3018, Ap
C 694	7	36.8	19	7	US-11-339-785-7	Sequence 7, App1.1	C 767	7	36.8	19	9	US-11-217-936-3032	Sequence 3032, Ap
C 695	7	36.8	19	7	US-11-344-702-36	Sequence 36, App1	C 768	7	36.8	19	9	US-11-217-936-3095	Sequence 3095, Ap
C 696	7	36.8	19	7	US-11-344-702-37	Sequence 37, App1	C 769	7	36.8	19	9	US-11-217-936-3162	Sequence 3162, Ap
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C 699	7	36.8	19	7	US-11-644-702-278	Sequence 278, App	C 772	7	36.8	19	9	US-11-217-936-3465	Sequence 3465, Ap
C 700	7	36.8	19	7	US-11-344-702-420	Sequence 420, App	C 773	7	36.8	19	9	US-11-217-936-3535	Sequence 3535, Ap
C 701	7	36.8	19	7	US-11-344-702-452	Sequence 452, App	C 774	7	36.8	19	9	US-11-217-936-3585	Sequence 3585, Ap
C 702	7	36.8	19	7	US-11-344-702-669	Sequence 669, App	C 775	7	36.8	19	9	US-11-217-936-3621	Sequence 3621, Ap
C 703	7	36.8	19	7	US-11-345-361-36	Sequence 36, App1	C 776	7	36.8	19	9	US-11-217-936-3638	Sequence 3638, Ap
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C 705	7	36.8	19	7	US-11-345-361-53	Sequence 53, App1	C 778	7	36.8	19	9	US-11-217-936-4151	Sequence 4151, Ap
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C 740	7	36.8	19	9	US-11-217-936-229	Sequence 229, App	C 813	7	36.8	19	9	US-11-102-097-1235	Sequence 1235, App
C 741	7	36.8	19	9	US-11-217-936-412	Sequence 412, App	C 814	7	36.8	19	9	US-11-102-097-1447	Sequence 1447, App
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ALIGNMENTS

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RESULT 1
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; Sequence 39, Application US/10921554
; Publication No. US20060142226A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics, Inc.
; APPLICANT: Polisky, Barry
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfer
; TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic A
; FILE REFERENCE: 04-466-A (400.206)
; CURRENT APPLICATION NUMBER: US/10/921,554
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 10/864,044
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
; LENGTH: 19
; TYPE: RNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target/siNA sense
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Best Local Similarity 63.6%; Pred. No. 1.3e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 9 ATCTCTTAC 19
DB 6 AUCUCUUCAC 16
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; Sequence 139, Application US/10921554
; Publication No. US20060142226A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics, Inc.
; APPLICANT: Polisky, Barry
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfer
; TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic Ac
; FILE REFERENCE: 04-466-A (400.206)
; CURRENT APPLICATION NUMBER: US/10/921,554
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 10/864,044
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: PatentIn version 3.3
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; OTHER INFORMATION: Description of Artificial Sequence: Target/siNA sense
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Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 14 ATCTCTTAC 4
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; Sequence 5004, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
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; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 19
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized P
US-11-293-697-5004

Query Match          55.8%; Score 10.6; DB 8; Length 19;
Best Local Similarity 76.5%; Pred. No. 2.1e+04;
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; Sequence 416, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
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; LENGTH: 19
; TYPE: RNA
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; FEATURE:
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US-11-217-936-416

Query Match          52.6%; Score 10; DB 9; Length 19;
Best Local Similarity 55.6%; Pred. No. 4.6e+04;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CGCAGGTATCTCTTCA 18
        |||||
Db      2 CGCAUGUACCUCAUGCA 19

RESULT 5
US-11-217-936-526/C
; Sequence 526, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sitna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
```

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; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 526
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-526

Query Match          52.6%; Score 10; DB 9; Length 19;
Best Local Similarity 72.2%; Pred. No. 4.6e+04;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CGCAGGTATCTCTTCA 18
        |||||
Db      18 CGCATGTACTCATGCA 1

RESULT 6
US-11-217-936-1455
; Sequence 1455, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sitna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1455
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1455

Query Match          52.6%; Score 10; DB 9; Length 19;
Best Local Similarity 50.0%; Pred. No. 4.6e+04;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      8 TATCTCCTTC 17
        :||:|
Db      8 UAUCCUCCUCC 17

RESULT 7
US-11-217-936-1924/C
; Sequence 1924, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sitna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1924
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Synthetic
US-11-217-936-1924

Query Match 52.6%; Score 10; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TATCTCTTC 17
|||
DB 12 TATCTCTTC 3

RESULT 8
US-10-921-554-94

Sequence 94, Application US/10921554
Publication No. US2006014226A1
GENERAL INFORMATION:
APPLICANT: Sirta Therapeutics, Inc.
APPLICANT: Polisky, Barry

TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfer
TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic A
TITLE OF INVENTION: (sRNA)
FILE REFERENCE: 04-466-A (400.206)

CURRENT FILING DATE: 2004-08-19
PRIOR FILING DATE: 2004-08-19
PRIOR FILING DATE: 2004-06-09

PRIOR APPLICATION NUMBER: PCT/US04/16390
PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 10/826,966

PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 10/757,803
PRIOR FILING DATE: 2004-01-14

PRIOR APPLICATION NUMBER: US 10/720,448
PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 10/693,059

PRIOR FILING DATE: 2003-11-23
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT/US03/05028

PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 326
SOFTWARE: PatentIn version 3.3

SEQ ID NO 94
LENGTH: 19
TYPE: RNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target/sRNA sense

US-10-921-554-94

Query Match 51.6%; Score 9.8; DB 6; Length 19;
Best Local Similarity 53.8%; Pred. No. 5.9e+04;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGTATCTCTTCA 18
|||:|||||
DB 5 GGUGUCUCUCCA 17

RESULT 9
US-10-921-554-194/c

Sequence 194, Application US/10921554
Publication No. US2006014226A1
GENERAL INFORMATION:

APPLICANT: Sirta Therapeutics, Inc.
APPLICANT: Polisky, Barry

APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfer
TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic Ac
TITLE OF INVENTION: (sRNA)

FILE REFERENCE: 04-466-A (400.206)
CURRENT FILING DATE: 2004-08-19
PRIOR FILING DATE: 2004-08-19

PRIOR APPLICATION NUMBER: US 10/864,044
PRIOR FILING DATE: 2004-06-09
PRIOR APPLICATION NUMBER: PCT/US04/16390

PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 10/826,966
PRIOR FILING DATE: 2004-04-16

PRIOR APPLICATION NUMBER: US 10/757,803
PRIOR FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 10/720,448

PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 10/693,059
PRIOR FILING DATE: 2003-11-23

PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT/US03/05028

PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 326
SOFTWARE: PatentIn version 3.3

SEQ ID NO 194
LENGTH: 19
TYPE: RNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target/sRNA sense

US-10-921-554-194

Query Match 51.6%; Score 9.8; DB 6; Length 19;
Best Local Similarity 84.6%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGTATCTCTTCA 18
|||:|||||
DB 15 GGUGUCUCUCCA 3

RESULT 10
US-11-344-702-269

Sequence 269, Application US/11344702
Publication No. US20060172963A1
GENERAL INFORMATION:

APPLICANT: Shepard, Allan R.
APPLICANT: Chatterton, Jon E.
TITLE OF INVENTION: RNA1-MEDIATED INHIBITION OF OCULAR HYPERTENSION TARGETS

FILE REFERENCE: 45263-P008US1
CURRENT FILING DATE: 2006-02-01
PRIOR FILING DATE: 2005-02-01

PRIOR APPLICATION NUMBER: US 60/648,926
PRIOR FILING DATE: 2005-12-22
NUMBER OF SEQ ID NOS: 724

SOFTWARE: PatentIn version 3.3
SEQ ID NO 269
LENGTH: 19

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: TARGETING SEQUENCE
US-11-344-702-269

Query Match 51.6%; Score 9.8; DB 7; Length 19;
Best Local Similarity 84.6%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTATCTCCTTCAC 19
Db 5 GTATCTACTCTCAC 17

RESULT 11
US-11-344-702-270
; Sequence 270, Application US/11344702
; Publication No. US20060172963A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Allan R.
; APPLICANT: Chatterton, Jon E.
; APPLICANT: Clark, Abbot F.
; TITLE OF INVENTION: RNAI-MEDIATED INHIBITION OF OCULAR HYPERTENSION TARGETS
; FILE REFERENCE: 45263-P008US1
; CURRENT APPLICATION NUMBER: US/11/344,702
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: US 60/648,926
; PRIOR FILING DATE: 2005-02-01
; PRIOR APPLICATION NUMBER: US 60/753,364
; PRIOR FILING DATE: 2005-12-22
; NUMBER OF SEQ ID NOS: 724
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 270
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TARGETING SEQUENCE
US-11-344-702-270

Query Match 51.6%; Score 9.8; DB 7; Length 19;
Best Local Similarity 84.6%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTATCTCCTTCAC 19
Db 4 GTATCTACTCTCAC 16

RESULT 12
US-11-344-702-271
; Sequence 271, Application US/11344702
; Publication No. US20060172963A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Allan R.
; APPLICANT: Chatterton, Jon E.
; APPLICANT: Clark, Abbot F.
; TITLE OF INVENTION: RNAI-MEDIATED INHIBITION OF OCULAR HYPERTENSION TARGETS
; FILE REFERENCE: 45263-P008US1
; CURRENT APPLICATION NUMBER: US/11/344,702
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: US 60/648,926
; PRIOR FILING DATE: 2005-02-01
; PRIOR APPLICATION NUMBER: US 60/753,364
; PRIOR FILING DATE: 2005-12-22
; NUMBER OF SEQ ID NOS: 724
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 271
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TARGETING SEQUENCE
US-11-344-702-271

Query Match 51.6%; Score 9.8; DB 7; Length 19;
Best Local Similarity 84.6%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTATCTCCTTCAC 19
Db 3 GTATCTACTCTCAC 15

RESULT 13
US-11-345-361-269
; Sequence 269, Application US/11345361
; Publication No. US20060172965A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Allan R.
; APPLICANT: Chatterton, Jon E.
; APPLICANT: Clark, Abbot F.
; APPLICANT: Max, Martin B.
; TITLE OF INVENTION: RNAI-MEDIATED INHIBITION OF OCULAR TARGETS
; FILE REFERENCE: 45263-P008US2
; CURRENT APPLICATION NUMBER: US/11/345,361
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: US 60/648,926
; PRIOR FILING DATE: 2005-02-01
; PRIOR APPLICATION NUMBER: US 60/753,364
; PRIOR FILING DATE: 2005-12-22
; NUMBER OF SEQ ID NOS: 724
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 269
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TARGETING SEQUENCE
US-11-345-361-269

Query Match 51.6%; Score 9.8; DB 7; Length 19;
Best Local Similarity 84.6%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTATCTCCTTCAC 19
Db 5 GTATCTACTCTCAC 17

RESULT 14
US-11-345-361-270
; Sequence 270, Application US/11345361
; Publication No. US20060172965A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Allan R.
; APPLICANT: Chatterton, Jon E.
; APPLICANT: Clark, Abbot F.
; APPLICANT: Max, Martin B.
; TITLE OF INVENTION: RNAI-MEDIATED INHIBITION OF OCULAR TARGETS
; FILE REFERENCE: 45263-P008US2
; CURRENT APPLICATION NUMBER: US/11/345,361
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: US 60/648,926
; PRIOR FILING DATE: 2005-02-01
; PRIOR APPLICATION NUMBER: US 60/753,364
; PRIOR FILING DATE: 2005-12-22
; NUMBER OF SEQ ID NOS: 724
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 270
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TARGETING SEQUENCE
US-11-345-361-270

Query Match 51.6%; Score 9.8; DB 7; Length 19;
Best Local Similarity 84.6%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GATATCTCTTAC 19
| | | | |
Db 4 GATATCTCTTAC 16

RESULT 15
US-11-345-361-271
; Sequence 271, Application US/11345361
; Publication No. US20060172965A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Allan R.
; APPLICANT: Chatterton, Jon E.
; APPLICANT: Clark, Abbot F.
; TITLE OF INVENTION: RNAI-MEDIATED INHIBITION OF OCULAR TARGETS
; FILE REFERENCE: 45263-P0808U2
; CURRENT APPLICATION NUMBER: US/11/345,361
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: US 60/648,926
; PRIOR FILING DATE: 2005-02-01
; PRIOR APPLICATION NUMBER: US 60/753,364
; PRIOR FILING DATE: 2005-12-22
; NUMBER OF SEQ ID NOS: 724
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 271
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TARGETING SEQUENCE
US-11-345-361-271

Query Match 51.6%; Score 9.8; DB 9; Length 19;
Best Local Similarity 84.6%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GATATCTCTTAC 19
| | | | |
Db 3 GATATCTCTTAC 15

RESULT 16
US-11-217-936-98/c
; Sequence 98, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-98

Query Match 51.6%; Score 9.8; DB 9; Length 19;
Best Local Similarity 84.6%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GATATCTCTTAC 19
| | | | |
Db 19 GATATCTCTTAC 7

RESULT 17
US-11-217-936-213

; Sequence 213, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 213
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-213

Query Match 51.6%; Score 9.8; DB 9; Length 19;
Best Local Similarity 53.8%; Pred. No. 5.9e+04;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GATATCTCTTAC 19
| | | | |
Db 1 GUATCCCUUCAC 13

RESULT 18
US-11-217-936-2810/c
; Sequence 2810, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2810
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-2810

Query Match 51.6%; Score 9.8; DB 9; Length 19;
Best Local Similarity 84.6%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGGATATCTT 16
| | | | |
Db 15 ATGGATATCTT 3

RESULT 19
US-11-217-936-3037
; Sequence 3037, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant

```

; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAc) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3037
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-11-217-936-3037

Query Match          51.6%; Score 9.8; DB 9; Length 19;
Best Local Similarity 46.2%; Pred. No. 5.9e+04;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy      4  ACGGATCTCCTT 16
Db      5  AUGGUAUACCUU 17

RESULT 20
US-10-424-339-335/c
; Sequence 335, Application US/10424339
; Publication No. US20060127891A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Naesim
; APPLICANT: Haebertl, Peter
; APPLICANT: Chowitra, Bharat
; APPLICANT: Polisky, Barry
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 400/113 (MBHB03-388)
; CURRENT APPLICATION NUMBER: US/10/424,339
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: PCT/US 03/02510
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US 03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 1714
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 335
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense 1
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US-10-424-339-335

Query Match          50.5%; Score 9.6; DB 6; Length 19;
Best Local Similarity 46.2%; Pred. No. 7.7e+04;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4  ACGGATCTCCTT 19
Db      19  ACGGCTGCCCTTAC 4

RESULT 21
US-10-424-339-440
; Sequence 440, Application US/10424339
; Publication No. US20060127891A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Naesim
; APPLICANT: Haebertl, Peter
; APPLICANT: Chowitra, Bharat
; APPLICANT: Polisky, Barry
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 400/113 (MBHB03-388)
; CURRENT APPLICATION NUMBER: US/10/424,339
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: PCT/US 03/02510
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US 03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 1714
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 440
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; US-10-424-339-440

Query Match          50.5%; Score 9.6; DB 6; Length 19;
Best Local Similarity 62.5%; Pred. No. 7.7e+04;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      4  ACGGATCTCCTT 19
Db      1  ACGGCTGCCCTTAC 16

RESULT 22
US-11-102-097-517/c
; Sequence 517, Application US/11102097
; Publication No. US20060160759A1
; GENERAL INFORMATION:
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; APPLICANT: Chen, et al.
; TITLE OF INVENTION: Influenza Therapeutic
; FILE REFERENCE: 0492611-0621
; CURRENT APPLICATION NUMBER: US/11/102,097
; CURRENT FILING DATE: 2005-04-08
; NUMBER OF SEQ ID NOS: 2326
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 517
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequences of functional target portions for RNAi to inhibit
; OTHER INFORMATION: Influenza virus.
; US-11-102-097-517

Query Match
Best Local Similarity 50.5%; Score 9.6; DB 9; Length 19;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTTC 17
Db 17 GCCCAGTACTGCTTC 2

RESULT 23
US-11-256-694-308
; Sequence 308, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
; US-11-256-694-308

Query Match
Best Local Similarity 49.5%; Score 9.4; DB 8; Length 19;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTTCA 18
Db 3 TATCTACTTCA 13

RESULT 24
US-11-256-694-319
; Sequence 319, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 319
```

```

; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
; US-11-256-694-319

Query Match
Best Local Similarity 49.5%; Score 9.4; DB 8; Length 19;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTTCA 18
Db 3 TATCTACTTCA 13

RESULT 25
US-11-256-694-332
; Sequence 332, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
; US-11-256-694-332

Query Match
Best Local Similarity 49.5%; Score 9.4; DB 8; Length 19;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTTCA 18
Db 3 TATCTACTTCA 13

RESULT 26
US-11-256-694-333
; Sequence 333, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 333
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
; US-11-256-694-333

Query Match
Best Local Similarity 49.5%; Score 9.4; DB 8; Length 19;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTTCA 18
Db 3 TATCTACTTCA 13
```

```
Db      3  TATCTACTTCA 13

RESULT 27
US-11-256-694-340
; Sequence 340, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundeborg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; PRIOR FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 340
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-11-256-694-340

Query Match      49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      8  TATCTCTTCA 18
        |||||
        3  TATCTACTTCA 13

RESULT 28
US-11-256-694-351
; Sequence 351, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundeborg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; PRIOR FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 351
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-11-256-694-351

Query Match      49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      8  TATCTCTTCA 18
        |||||
        3  TATCTACTTCA 13

RESULT 29
US-11-256-694-362
; Sequence 362, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundeborg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; PRIOR FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 362
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-11-256-694-362

Query Match      49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      8  TATCTCTTCA 18
        |||||
        3  TATCTACTTCA 13

TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; PRIOR FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 362
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-11-256-694-362

Query Match      49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      8  TATCTCTTCA 18
        |||||
        3  TATCTACTTCA 13

RESULT 30
US-11-256-694-373
; Sequence 373, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundeborg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; PRIOR FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 373
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-11-256-694-373

Query Match      49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      8  TATCTCTTCA 18
        |||||
        3  TATCTACTTCA 13

RESULT 31
US-11-256-694-384
; Sequence 384, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundeborg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; PRIOR FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 384
; LENGTH: 19
; TYPE: DNA
```

; ORGANISM: Human papillomavirus
US-11-256-694-384

Query Match 49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTTCA 18
|||||
Db 3 TATCTACTTCA 13

RESULT 32
US-11-256-694-395

; Sequence 395, Application US/11256694
; Publication No. US2006008872A1
; GENERAL INFORMATION:

; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 395
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-11-256-694-395

Query Match 49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTTCA 18
|||||
Db 3 TATCTACTTCA 13

RESULT 33
US-11-256-694-406

; Sequence 406, Application US/11256694
; Publication No. US2006008872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 406
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-11-256-694-406

Query Match 49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTTCA 18
|||||
Db 3 TATCTACTTCA 13

RESULT 34
US-11-217-936-727/C

; Sequence 727, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 727
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Synthetic
US-11-217-936-727

Query Match 49.5%; Score 9.4; DB 9; Length 19;
Best Local Similarity 68.4%; Pred. No. 9.9e+04;
Matches 13; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTCAC 19
|||||
Db 19 CGGACAGTATACACACAC 1

RESULT 35
US-11-217-936-835

; Sequence 835, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 835
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Synthetic
US-11-217-936-835

Query Match 49.5%; Score 9.4; DB 9; Length 19;
Best Local Similarity 57.9%; Pred. No. 9.9e+04;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTCAC 19
|||:|:|
Db 1 CGGACAGTATACACACAC 19

RESULT 36
US-10-825-485-284

; Sequence 284, Application US/10825485
; Publication No. US20060160757A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.


```
APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hairless (HR) Gene
; TITLE OF INVENTION: Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/150 (MHB04-378)
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US/10/825,485
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 724
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 284
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-825-485-284

Query Match          48.4%; Score 9.2; DB 6; Length 19;
Best Local Similarity 64.3%; Pred. No. 1.3e+05;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      6 GGATCTCTCTTAC 19
        |||:|||||
Db      2 GGCAUUCUCCCCAC 15

RESULT 37
US-10-825-485-591/c
; Sequence 591, Application US/10825485
; Publication No. US20060160757A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hairless (HR) Gene
; TITLE OF INVENTION: Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/150 (MHB04-378)
; CURRENT APPLICATION NUMBER: US/10/825,485
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
```

```
PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 724
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 591
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-825-485-591

Query Match          48.4%; Score 9.2; DB 6; Length 19;
Best Local Similarity 78.6%; Pred. No. 1.3e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 GGATCTCTCTTAC 19
        |||:|||||
Db      18 GGATCTCTCTTAC 5

RESULT 38
US-11-251-465-467/c
; Sequence 467, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brye, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-467

Query Match          48.4%; Score 9.2; DB 8; Length 19;
Best Local Similarity 78.6%; Pred. No. 1.3e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 CGGTAATCTCTTCA 18
        |||:|||||
Db      17 CTGTGTCTGTCTCA 4

RESULT 39
US-11-217-936-1014/c
; Sequence 1014, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 05-727 (400/271)
```

```

; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1014
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1014

```

```

Query Match          48.4%; Score 9.2; DB 9; Length 19;
Best Local Similarity 78.6%; Pred. No. 1.3e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 CGCAGCGTATCTCC 14
          |||||
DB      14 CGCGCCGCAUCC 1

```

```

RESULT 40
US-11-217-936-1483
; Sequence 1483, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1483
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1483

```

```

Query Match          48.4%; Score 9.2; DB 9; Length 19;
Best Local Similarity 64.3%; Pred. No. 1.3e+05;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 CGCAGCGTATCTCC 14
          |||||
DB      6 CGCGCCGCAUCC 19

```

Search completed: August 10, 2006, 09:26:45
 Job time : 91.3333 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 08:42:03 ; Search time 1823.67 Seconds
(without alignments)
582.600 Million cell updates/sec

Title: US-10-636-065-29

Perfect score: 19

Sequence: 1 cgcacgctacctcttcac 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 3374

Minimum DB seq length: 19

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	10.8	56.8	19	13	CL671134 PRI0163d
C 2	9.8	51.6	19	11	AZ481008 IM0302N15
C 3	8.6	45.3	19	11	AZ309116 IM0012E23
C 4	8.4	44.2	19	5	CF317235 HD--06-N1
C 5	8.2	43.2	19	5	CF929669 CF--01-R-E
C 6	8.2	43.2	19	14	AJ840508 Arabidops
C 7	8	42.1	19	5	CD532073 13104 Ara
C 8	8	42.1	19	5	CF280788 14ETL--07
C 9	8	42.1	19	5	CF299371 7LEAF--03
C 10	8	42.1	19	5	CF305417 GLEAF--01
C 11	8	42.1	19	5	CF315940 HD--05-A1
C 12	8	42.1	19	5	CF337272 JMT--07-K
C 13	8	42.1	19	11	AZ506614 IM0347A24
C 14	8	42.1	19	13	AZ995903 2M0281H19
C 15	8	42.1	19	13	CL657608 PRI012a_B
C 16	8	42.1	19	14	AJ587912 Arabidops
C 17	8	42.1	19	14	AJ600880 Arabidops
C 18	7.8	41.1	19	11	AZ308865 IM0012M14
C 19	7.8	41.1	19	11	AZ313113 IM0029N17

C 20	7.8	41.1	19	11	AZ411858	AZ411858 IM0185P01
C 21	7.8	41.1	19	11	AZ514774	AZ514774 IM0361N11
C 22	7.8	41.1	19	11	AZ585898	AZ585898 IM0391L22
C 23	7.8	41.1	19	11	AZ643528	AZ643528 IM0507H05
C 24	7.6	40.0	19	14	AJ587549	AJ587549 Arabidops
C 25	7.6	40.0	19	5	CF281537	CF281537 14ETL--08
C 26	7.6	40.0	19	9	DR026632	DR026632 Osmo01180
C 27	7.6	40.0	19	11	AZ314603	AZ314603 IM0031C06
C 28	7.6	40.0	19	11	AZ505490	AZ505490 IM0346N08
C 29	7.6	40.0	19	11	AZ582154	AZ582154 IM0374C19
C 30	7.6	40.0	19	11	AZ627164	AZ627164 2M0103M22
C 31	7.4	38.9	19	1	A1663799	A1663799 u106a10.x
C 32	7.4	38.9	19	9	DN955351	DN955351 iEB6d05.g
C 33	7.4	38.9	19	11	AZ329293	AZ329293 IM0053A03
C 34	7.4	38.9	19	11	AZ443948	AZ443948 IM0238P04
C 35	7.4	38.9	19	11	AZ484016	AZ484016 IM0310J10
C 36	7.4	38.9	19	11	AZ500675	AZ500675 IM0339J10
C 37	7.4	38.9	19	11	AZ634038	AZ634038 2M0116H01
C 38	7.4	38.9	19	14	AJ597721	AJ597721 Arabidops
C 39	7.2	37.9	19	1	AM075504	AM075504 AM075504
C 40	7.2	37.9	19	4	BX560116	BX560116 BX560116
C 41	7.2	37.9	19	11	AZ315768	AZ315768 IM0033F01
C 42	7.2	37.9	19	11	AZ341880	AZ341880 IM0074O04
C 43	7.2	37.9	19	11	AZ420252	AZ420252 IM0198G01
C 44	7.2	37.9	19	11	AZ612157	AZ612157 IM0438L21
C 45	7.2	37.9	19	11	AZ636789	AZ636789 2M0211I18
C 46	7.2	37.9	19	11	AJ599121	AJ599121 Arabidops
C 47	7	36.8	19	2	BM398839	BM398839 5009-0-5-
C 48	7	36.8	19	5	CF276559	CF276559 14ETL--01
C 49	7	36.8	19	11	AZ413045	AZ413045 IM0168H19
C 50	7	36.8	19	11	AZ429998	AZ429998 IM0214F16
C 51	7	36.8	19	11	AZ447414	AZ447414 IM0244L06
C 52	7	36.8	19	11	AZ585367	AZ585367 IM0390D06
C 53	7	36.8	19	11	AZ783569	AZ783569 2M0055J28
C 54	7	36.8	19	11	AZ799394	AZ799394 2M0055J28
C 55	7	36.8	19	11	AZ966788	AZ966788 2M0237O21
C 56	7	36.8	19	13	CL423580	CL423580 O1S0557-0
C 57	7	36.8	19	14	AJ587242	AJ587242 Arabidops
C 58	6.8	35.8	19	2	BM397268	BM397268 5009-0-30
C 59	6.8	35.8	19	5	CD530354	CD530354 O5N18 Ara
C 60	6.8	35.8	19	8	CO780487	CO780487 BL009D BO
C 61	6.8	35.8	19	8	CO781533	CO781533 BL012C HO
C 62	6.8	35.8	19	8	CO781533	CO781533 BL012C HO
C 63	6.8	35.8	19	8	CO781533	CO781533 BL012C HO
C 64	6.8	35.8	19	11	AZ372219	AZ372219 IM0154B03
C 65	6.8	35.8	19	11	AZ380009	AZ380009 IM0154L19
C 66	6.8	35.8	19	11	AZ422531	AZ422531 IM0201B16
C 67	6.8	35.8	19	11	AZ432757	AZ432757 IM0218L14
C 68	6.8	35.8	19	11	AZ440413	AZ440413 IM0231A01
C 69	6.8	35.8	19	11	AZ450047	AZ450047 IM0248A08
C 70	6.8	35.8	19	11	AZ490174	AZ490174 IM0323B05
C 71	6.8	35.8	19	11	AZ510122	AZ510122 IM0354K20
C 72	6.8	35.8	19	11	AZ514405	AZ514405 IM0361L03
C 73	6.8	35.8	19	11	AZ608373	AZ608373 IM0432E01
C 74	6.8	35.8	19	11	AZ774205	AZ774205 2M0003P13
C 75	6.8	35.8	19	11	AZ801563	AZ801563 2M006C011
C 76	6.8	35.8	19	11	AZ827092	AZ827092 2M0103M18
C 77	6.8	35.8	19	11	AZ854740	AZ854740 2M0158C01
C 78	6.8	35.8	19	11	AZ949895	AZ949895 2M0213N08
C 79	6.8	35.8	19	11	AZ983014	AZ983014 2M0264H02
C 80	6.8	35.8	19	14	AJ589865	AJ589865 Arabidops
C 81	6.8	35.8	19	14	AJ589865	AJ589865 Arabidops
C 82	6.6	34.7	19	1	A1569191	A1569191 t-83f12.x
C 83	6.6	34.7	19	1	A1569191	A1569191 t-83f12.x
C 84	6.6	34.7	19	3	BO593607	BO593607 E012766-0
C 85	6.6	34.7	19	4	CO1186	CO1186 HUMGS000788
C 86	6.6	34.7	19	5	CF109555	CF109555 ABE--03-M
C 87	6.6	34.7	19	7	AM250655	AM250655 2822262.5
C 88	6.6	34.7	19	9	DN954542	DN954542 t-74e12.9
C 89	6.6	34.7	19	9	DN954542	DN954542 t-74e12.9
C 90	6.6	34.7	19	11	AZ303767	AZ303767 IM0003C03
C 91	6.6	34.7	19	11	AZ335373	AZ335373 IM0065J16
C 92	6.6	34.7	19	11	AZ355195	AZ355195 IM0094G22

C 93	6.6	34.7	19 11	A2452087	A2452087 1M0251F18	C 166	6	31.6	19 2	BM396507	5009-0-21
C 94	6.6	34.7	19 11	A2772174	A2772174 1M0574C22	C 167	6	31.6	19 2	BM397047	5009-0-28
C 95	6.6	34.7	19 11	A2782026	A2782026 2M0021123	C 168	6	31.6	19 2	BM398909	5009-0-50
C 96	6.6	34.7	19 11	A2810697	A2810697 2M0076M17	C 169	6	31.6	19 2	BM399219	5009-0-55
C 97	6.6	34.7	19 11	A2859982	A2859982 2M0227L13	C 170	6	31.6	19 4	BK555622	BK555622
C 98	6.6	34.7	19 11	A2893624	A2893624 2M0264A22	C 171	6	31.6	19 4	C02594	C02594
C 99	6.6	33.7	19 14	AJ587349	AJ587349 ArbiIdops	C 172	6	31.6	19 5	C21102	C21102
C 100	6.4	33.7	19 1	A1208797	A1208797 q944E07.x	C 173	6	31.6	19 5	CD533717	CD533717
C 101	6.4	33.7	19 1	A1545076	A1545076 FB70d07.Y	C 174	6	31.6	19 5	CP294117	CP294117
C 102	6.4	33.7	19 1	A1747751	A1747751 u121b05.x	C 175	6	31.6	19 5	CP328201	CP328201
C 103	6.4	33.7	19 1	AJ660242	AJ660242 AJ660242	C 176	6	31.6	19 5	CP340173	CP340173
C 104	6.4	33.7	19 1	AJ660794	AJ660794 AJ660794	C 177	6	31.6	19 8	CP0792214	CP0792214
C 105	6.4	33.7	19 1	AJ661104	AJ661104 AJ661104	C 178	6	31.6	19 9	DR105341	DR105341
C 106	6.4	33.7	19 1	AJ671616	AJ671616 AJ671616	C 179	6	31.6	19 11	A2330741	A2330741
C 107	6.4	33.7	19 1	AJ687665	AJ687665 AJ687665	C 180	6	31.6	19 11	A2369420	A2369420
C 108	6.4	33.7	19 3	B0594129	B0594129 E012759-0	C 181	6	31.6	19 11	A2394192	A2394192
C 109	6.4	33.7	19 4	C01216	C01216 HUMS000792	C 182	6	31.6	19 11	A2403537	A2403537
C 110	6.4	33.7	19 8	C0783138	C0783138 BL017A_G0	C 183	6	31.6	19 11	A2411255	A2411255
C 111	6.4	33.7	19 8	C0788716	C0788716 NT005A_A0	C 184	6	31.6	19 11	A2413276	A2413276
C 112	6.4	33.7	19 8	CV933688	CV933688 PMpcm_35	C 185	6	31.6	19 11	A2446934	A2446934
C 113	6.4	33.7	19 9	D17097	D17097 D17097_K1ee	C 186	6	31.6	19 11	A2460812	A2460812
C 114	6.4	33.7	19 9	AZ307686	AZ307686 1M0009B05	C 187	6	31.6	19 11	A2466784	A2466784
C 115	6.4	33.7	19 11	AZ346687	AZ346687 1M0082J06	C 188	6	31.6	19 11	A2495417	A2495417
C 116	6.4	33.7	19 11	AZ466725	AZ466725 1M0277C09	C 189	6	31.6	19 11	A2514408	A2514408
C 117	6.4	33.7	19 11	AZ477382	AZ477382 1M0296P16	C 190	6	31.6	19 11	A2589109	A2589109
C 118	6.4	33.7	19 11	AZ481877	AZ481877 1M0306B01	C 191	6	31.6	19 11	A2597219	A2597219
C 119	6.4	33.7	19 11	AZ491592	AZ491592 1M0325P16	C 192	6	31.6	19 11	A2615728	A2615728
C 120	6.4	33.7	19 11	AZ494890	AZ494890 1M0330N19	C 193	6	31.6	19 11	A2646713	A2646713
C 121	6.4	33.7	19 11	AZ623663	AZ623663 1M0461B07	C 194	6	31.6	19 11	A2659427	A2659427
C 122	6.4	33.7	19 11	AZ663240	AZ663240 1M0542H18	C 195	6	31.6	19 11	A2769407	A2769407
C 123	6.4	33.7	19 11	AZ71143	AZ71143 1M0573A07	C 196	6	31.6	19 11	A2776860	A2776860
C 124	6.4	33.7	19 11	AZ781954	AZ781954 2M0021F17	C 197	6	31.6	19 11	A2779094	A2779094
C 125	6.4	33.7	19 11	AZ783702	AZ783702 2M0025I08	C 198	6	31.6	19 11	A2781587	A2781587
C 126	6.4	33.7	19 11	AZ825898	AZ825898 2M0101O18	C 199	6	31.6	19 11	A2821649	A2821649
C 127	6.2	32.6	19 1	AJ662141	AJ662141 AJ662141	C 200	6	31.6	19 11	A2824929	A2824929
C 128	6.2	32.6	19 1	AJ696907	AJ696907 AJ696907	C 201	6	31.6	19 11	A2854025	A2854025
C 129	6.2	32.6	19 1	AJ696991	AJ696991 PRODIGI0D	C 202	6	31.6	19 11	A2857450	A2857450
C 130	6.2	32.6	19 3	BU101840	BU101840 HD--08-12	C 203	6	31.6	19 11	CL663550	CL663550
C 131	6.2	32.6	19 5	CF318426	CF318426 NT010A_G0	C 204	6	31.6	19 11	CL683526	CL683526
C 132	6.2	32.6	19 8	CO790624	CO790624 NT010A_G0	C 205	6	31.6	19 13	CL683526	CL683526
C 133	6.2	32.6	19 9	DN475867	DN475867 A1E202Xa	C 206	6	31.6	19 13	CL683526	CL683526
C 134	6.2	32.6	19 11	AZ313035	AZ313035 1M0029P10	C 207	6	31.6	19 14	AJ587173	AJ587173
C 135	6.2	32.6	19 11	AZ424633	AZ424633 1M0204J24	C 208	6	31.6	19 14	AJ587186	AJ587186
C 136	6.2	32.6	19 11	AZ441505	AZ441505 1M0233M13	C 209	6	31.6	19 14	AJ591165	AJ591165
C 137	6.2	32.6	19 11	AZ489586	AZ489586 1M0322C12	C 210	6	31.6	19 14	ATH529932	ATH529932
C 138	6.2	32.6	19 11	AZ500053	AZ500053 1M0338M08	C 211	6	31.6	19 14	AA918795	AA918795
C 139	6.2	32.6	19 11	AZ500608	AZ500608 1M0339L05	C 212	6	30.5	19 1	A1371092	A1371092
C 140	6.2	32.6	19 11	AZ502110	AZ502110 1M0341C18	C 213	6	30.5	19 1	A1500684	A1500684
C 141	6.2	32.6	19 11	AZ510143	AZ510143 1M0354P21	C 214	6	30.5	19 1	A1664013	A1664013
C 142	6.2	32.6	19 11	AZ610584	AZ610584 1M0435P20	C 215	6	30.5	19 1	A1687565	A1687565
C 143	6.2	32.6	19 11	AZ663744	AZ663744 1M0543J01	C 216	6	30.5	19 1	AJ061154	AJ061154
C 144	6.2	32.6	19 11	AZ664265	AZ664265 1M0544A19	C 217	6	30.5	19 1	BM395903	BM395903
C 145	6.2	32.6	19 11	AZ785573	AZ785573 2M0029L02	C 218	6	30.5	19 2	BO599374	BO599374
C 146	6.2	32.6	19 11	AZ805949	AZ805949 2M0067F07	C 219	6	30.5	19 3	CP2818784	CP2818784
C 147	6.2	32.6	19 11	AZ806283	AZ806283 2M0068A16	C 220	6	30.5	19 3	CP298134	CP298134
C 148	6.2	32.6	19 11	AZ808212	AZ808212 2M0071D03	C 221	6	30.5	19 5	CP306225	CP306225
C 149	6.2	32.6	19 11	AZ815827	AZ815827 2M0084K23	C 222	6	30.5	19 5	CP307006	CP307006
C 150	6.2	32.6	19 11	AZ834038	AZ834038 2M0116H01	C 223	6	30.5	19 5	CP307439	CP307439
C 151	6.2	32.6	19 11	AZ842166	AZ842166 2M0140G06	C 224	6	30.5	19 5	CP3077507	CP3077507
C 152	6.2	32.6	19 11	AZ861634	AZ861634 2M0168B18	C 225	6	30.5	19 5	CP308022	CP308022
C 153	6.2	32.6	19 11	AZ949895	AZ949895 2M0213N08	C 226	6	30.5	19 5	CP3085345	CP3085345
C 154	6.2	32.6	19 11	AZ956423	AZ956423 2M0222F24	C 227	6	30.5	19 8	CP30937214	CP30937214
C 155	6.2	32.6	19 13	CL678657	CL678657 PR10123C	C 228	6	30.5	19 8	CP3094173	CP3094173
C 156	6.2	32.6	19 14	AJ588791	AJ588791 ArbiIdops	C 229	6	30.5	19 8	CP340173	CP340173
C 157	6.2	32.6	19 14	TA11B08F	TA11B08F T. BruceI	C 230	6	30.5	19 9	CP340173	CP340173
C 158	6	31.6	19 1	A1120725	A1120725 uB72B11.r	C 231	6	30.5	19 9	CP340173	CP340173
C 159	6	31.6	19 1	A1142547	A1142547 qd47D08.x	C 232	6	30.5	19 11	CP340173	CP340173
C 160	6	31.6	19 1	A1155325	A1155325 uB88A05.r	C 233	6	30.5	19 11	CP340173	CP340173
C 161	6	31.6	19 1	AJ920596	AJ920596 5009-0-11	C 234	6	30.5	19 11	CP340173	CP340173
C 162	6	31.6	19 2	BM395769	BM395769 5009-0-11	C 235	6	30.5	19 11	CP340173	CP340173
C 163	6	31.6	19 2	BM395792	BM395792 5009-0-11	C 236	6	30.5	19 11	CP340173	CP340173
C 164	6	31.6	19 2	BM396264	BM396264 5009-0-19	C 237	6	30.5	19 11	CP340173	CP340173
C 165	6	31.6	19 2	BM396331	BM396331 5009-0-2-	C 238	6	30.5	19 11	CP340173	CP340173

239	5.8	30.5	19	11	AZ345527	AZ345527	1M0080N02	C 312	5.6	29.5	19	1	AJ652627	AJ652627
240	5.8	30.5	19	11	AZ345536	AZ345536	1M0080O06	313	5.6	29.5	19	1	AJ657936	AJ657936
241	5.8	30.5	19	11	AZ345572	AZ345572	1M0080U17	314	5.6	29.5	19	1	AJ666284	AJ666284
242	5.8	30.5	19	11	AZ346709	AZ346709	1M0082M06	315	5.6	29.5	19	2	BM396413	BM396413
243	5.8	30.5	19	11	AZ346710	AZ346710	1M0082N01	316	5.6	29.5	19	2	BM396814	BM396814
244	5.8	30.5	19	11	AZ357983	AZ357983	1M0099J19	C 317	5.6	29.5	19	2	BM398524	BM398524
245	5.8	30.5	19	11	AZ360332	AZ360332	1M0103J04	C 318	5.6	29.5	19	2	BM399274	BM399274
246	5.8	30.5	19	11	AZ368655	AZ368655	1M0118P13	C 319	5.6	29.5	19	2	BM400783	BM400783
247	5.8	30.5	19	11	AZ368837	AZ368837	1M0119A11	C 320	5.6	29.5	19	2	BM401020	BM401020
248	5.8	30.5	19	11	AZ371083	AZ371083	1M0123C01	C 321	5.6	29.5	19	3	BM583648	BM583648
249	5.8	30.5	19	11	AZ372854	AZ372854	1M0124G22	C 322	5.6	29.5	19	3	BM589692	BM589692
250	5.8	30.5	19	11	AZ375581	AZ375581	1M0129E05	C 323	5.6	29.5	19	3	BM593604	BM593604
C 251	5.8	30.5	19	11	AZ386717	AZ386717	1M0145P17	C 324	5.6	29.5	19	4	CO25594	CO25594
C 252	5.8	30.5	19	11	AZ387157	AZ387157	1M0146B20	C 325	5.6	29.5	19	5	CF297283	CF297283
C 253	5.8	30.5	19	11	AZ393054	AZ393054	1M0155N21	C 326	5.6	29.5	19	5	CF305339	CF305339
C 254	5.8	30.5	19	11	AZ407748	AZ407748	1M0178C07	327	5.6	29.5	19	5	CK576562	CK576562
C 255	5.8	30.5	19	11	AZ410166	AZ410166	1M0182J17	C 328	5.6	29.5	19	7	AM248167	AM248167
256	5.8	30.5	19	11	AZ445563	AZ445563	1M0241P18	C 329	5.6	29.5	19	8	CO778963	CO778963
257	5.8	30.5	19	11	AZ447223	AZ447223	1M0244H13	C 330	5.6	29.5	19	8	CO779910	CO779910
258	5.8	30.5	19	11	AZ447247	AZ447247	1M0244G19	C 331	5.6	29.5	19	8	CO780487	CO780487
259	5.8	30.5	19	11	AZ452087	AZ452087	1M0251F18	C 332	5.6	29.5	19	8	CO781979	CO781979
260	5.8	30.5	19	11	AZ463791	AZ463791	1M0272C22	C 333	5.6	29.5	19	8	CO790444	CO790444
C 261	5.8	30.5	19	11	AZ463791	AZ463791	1M0272C22	C 334	5.6	29.5	19	8	CO793357	CO793357
262	5.8	30.5	19	11	AZ470220	AZ470220	1M0284M11	C 335	5.6	29.5	19	9	DR062800	DR062800
263	5.8	30.5	19	11	AZ480415	AZ480415	1M0301K24	C 336	5.6	29.5	19	9	DR103208	DR103208
264	5.8	30.5	19	11	AZ489350	AZ489350	1M0321K14	C 337	5.6	29.5	19	11	AZ309531	AZ309531
265	5.8	30.5	19	11	AZ510096	AZ510096	1M0354B22	C 338	5.6	29.5	19	11	AZ314110	AZ314110
266	5.8	30.5	19	11	AZ510106	AZ510106	1M0354E19	C 339	5.6	29.5	19	11	AZ316210	AZ316210
267	5.8	30.5	19	11	AZ510952	AZ510952	1M0355G15	C 340	5.6	29.5	19	11	AZ317020	AZ317020
268	5.8	30.5	19	11	AZ517956	AZ517956	1M0367L08	C 341	5.6	29.5	19	11	AZ323590	AZ323590
C 269	5.8	30.5	19	11	AZ579566	AZ579566	1M0367L08	C 342	5.6	29.5	19	11	AZ340126	AZ340126
C 270	5.8	30.5	19	11	AZ585820	AZ585820	1M0391I15	C 343	5.6	29.5	19	11	AZ346629	AZ346629
271	5.8	30.5	19	11	AZ611716	AZ611716	1M0438B15	C 344	5.6	29.5	19	11	AZ359508	AZ359508
C 272	5.8	30.5	19	11	AZ614702	AZ614702	1M0443F10	345	5.6	29.5	19	11	AZ612624	AZ612624
C 273	5.8	30.5	19	11	AZ626573	AZ626573	1M0466J24	346	5.6	29.5	19	11	AZ613058	AZ613058
C 274	5.8	30.5	19	11	AZ626779	AZ626779	1M0467A14	347	5.6	29.5	19	11	AZ637711	AZ637711
275	5.8	30.5	19	11	AZ634666	AZ634666	1M0490P03	348	5.6	29.5	19	11	AZ641145	AZ641145
C 276	5.8	30.5	19	11	AZ638980	AZ638980	1M0499L08	349	5.6	29.5	19	11	AZ655972	AZ655972
277	5.8	30.5	19	11	AZ647364	AZ647364	1M05130A6	350	5.6	29.5	19	11	AZ771560	AZ771560
C 278	5.8	30.5	19	11	AZ663184	AZ663184	1M0542L07	C 351	5.6	29.5	19	11	AZ772819	AZ772819
C 279	5.8	30.5	19	11	AZ663184	AZ663184	1M0542L07	C 352	5.6	29.5	19	11	AZ782308	AZ782308
C 280	5.8	30.5	19	11	AZ759494	AZ759494	1M0552K06	353	5.6	29.5	19	11	AZ783477	AZ783477
C 281	5.8	30.5	19	11	AZ761740	AZ761740	1M0556A13	354	5.6	29.5	19	11	AZ822713	AZ822713
C 282	5.8	30.5	19	11	AZ769232	AZ769232	1M0569H07	355	5.6	29.5	19	11	AZ826447	AZ826447
C 283	5.8	30.5	19	11	AZ769437	AZ769437	1M0570A07	C 356	5.6	29.5	19	11	AZ860660	AZ860660
C 284	5.8	30.5	19	11	AZ774950	AZ774950	2M0004M16	C 357	5.6	29.5	19	11	AZ874357	AZ874357
C 285	5.8	30.5	19	11	AZ775460	AZ775460	2M0008H15	C 358	5.6	29.5	19	11	AZ936396	AZ936396
286	5.8	30.5	19	11	AZ784061	AZ784061	2M0026M20	359	5.6	29.5	19	11	AZ974357	AZ974357
287	5.8	30.5	19	11	AZ786336	AZ786336	2M0031H17	C 360	5.6	29.5	19	11	AZ976225	AZ976225
C 288	5.8	30.5	19	11	AZ790121	AZ790121	2M0038P21	C 361	5.6	29.5	19	13	CU878326	CU878326
C 289	5.8	30.5	19	11	AZ792979	AZ792979	2M0046G04	362	5.6	29.5	19	14	AJ599527	AJ599527
C 290	5.8	30.5	19	11	AZ795136	AZ795136	2M0049A16	363	5.4	28.4	19	1	AA916934	AA916934
C 291	5.8	30.5	19	11	AZ799463	AZ799463	2M0057A01	C 364	5.4	28.4	19	1	AI027323	AI027323
C 292	5.8	30.5	19	11	AZ800056	AZ800056	2M0057E20	365	5.4	28.4	19	1	AI147066	AI147066
C 293	5.8	30.5	19	11	AZ807034	AZ807034	2M0069B05	366	5.4	28.4	19	1	AI183836	AI183836
C 294	5.8	30.5	19	11	AZ820818	AZ820818	2M0093I18	C 367	5.4	28.4	19	1	AI183934	AI183934
C 295	5.8	30.5	19	11	AZ823855	AZ823855	2M0095F09	C 368	5.4	28.4	19	1	AI1965637	AI1965637
C 296	5.8	30.5	19	11	AZ832928	AZ832928	2M0113U08	C 369	5.4	28.4	19	1	AI696833	AI696833
C 297	5.8	30.5	19	11	AZ838444	AZ838444	2M0116O07	370	5.4	28.4	19	1	AI790036	AI790036
C 298	5.8	30.5	19	11	AZ842379	AZ842379	2M0140N17	371	5.4	28.4	19	1	AI811474	AI811474
C 299	5.8	30.5	19	11	AZ864822	AZ864822	2M0174C08	372	5.4	28.4	19	1	AJ552663	AJ552663
300	5.8	30.5	19	11	AZ936396	AZ936396	2M0193M02	C 373	5.4	28.4	19	1	AJ746804	AJ746804
301	5.8	30.5	19	11	AZ949954	AZ949954	2M0213J16	C 374	5.4	28.4	19	1	AM075572	AM075572
302	5.8	30.5	19	11	AZ951124	AZ951124	2M0215A02	C 375	5.4	28.4	19	1	BM396949	BM396949
C 303	5.8	30.5	19	11	AZ968667	AZ968667	2M0241A07	376	5.4	28.4	19	1	BM3995169	BM3995169
304	5.8	30.5	19	11	AZ991837	AZ991837	2M0276E17	377	5.4	28.4	19	2	BM395903	BM395903
C 305	5.8	30.5	19	14	AJ587349	AJ587349	ArabiIdops	378	5.4	28.4	19	2	BM396766	BM396766
C 306	5.8	30.5	19	14	AJ588602	AJ588602	ArabiIdops	379	5.4	28.4	19	2	BM399684	BM399684
C 307	5.8	30.5	19	14	AJ588965	AJ588965	ArabiIdops	C 380	5.4	28.4	19	2	BM587387	BM587387
C 308	5.8	30.5	19	14	AJ589255	AJ589255	ArabiIdops	C 381	5.4	28.4	19	3	BO582903	BO582903
C 309	5.8	30.5	19	14	AJ589873	AJ589873	ArabiIdops	382	5.4	28.4	19	3	BO587387	BO587387
C 310	5.8	30.5	19	14	AJ601030	AJ601030	ArabiIdops	C 383	5.4	28.4	19	3	CO1186	CO1186
C 311	5.8	30.5	19	14	ATH527470	ATH527470	ArabiIdops	C 384	5.4	28.4	19	4	CO1186	CO1186

C 385	5.4	28.4	19	4	CO1584	C01584	HUMG000858	458	5.4	28.4	19	11	A2778302	A2778302	2M0013C02
C 386	5.4	28.4	19	4	CA587820	CA587820	LBRI6P60	C 459	5.4	28.4	19	11	A2780833	A2780833	2M0018M21
C 387	5.4	28.4	19	4	CB413855	CB413855	ScAE_2576	C 460	5.4	28.4	19	11	A2783569	A2783569	2M0025O22
C 388	5.4	28.4	19	4	CB415466	CB415466	ScAE_4656	C 461	5.4	28.4	19	11	A2794440	A2794440	2M0048N15
C 389	5.4	28.4	19	5	CF294232	CF294232	30DG5--03	C 462	5.4	28.4	19	11	A2798425	A2798425	2M0055D13
C 390	5.4	28.4	19	5	CF298891	CF298891	7LEAF--02	C 463	5.4	28.4	19	11	A2803756	A2803756	2M0064M15
C 391	5.4	28.4	19	5	CF308262	CF308262	ABF--02-A	C 464	5.4	28.4	19	11	A2804026	A2804026	2M0064O07
C 392	5.4	28.4	19	5	CF311635	CF311635	ABF--06-O	C 465	5.4	28.4	19	11	A2809394	A2809394	2M0073B19
C 393	5.4	28.4	19	5	CF313581	CF313581	HD--01-M0	C 466	5.4	28.4	19	11	A2812572	A2812572	2M0079O15
C 394	5.4	28.4	19	5	CF316935	CF316935	HD--06-H0	C 467	5.4	28.4	19	11	A2822713	A2822713	2M0096M08
C 395	5.4	28.4	19	5	CF337608	CF337608	WJT--08-H0	C 468	5.4	28.4	19	11	A2832901	A2832901	2M0113P12
C 396	5.4	28.4	19	5	CF542982	CF542982	S014680w-	C 469	5.4	28.4	19	11	A2835928	A2835928	2M0113U08
C 397	5.4	28.4	19	6	CNS09MAX	CF542982	Single re	C 470	5.4	28.4	19	11	A2835034	A2835034	2M0129X04
C 398	5.4	28.4	19	8	CO790624	CO790624	NT010A_G0	C 471	5.4	28.4	19	11	A2847888	A2847888	2M0148G07
C 399	5.4	28.4	19	8	CO791279	CO791279	NT012A	C 472	5.4	28.4	19	11	A2854718	A2854718	2M0158M23
C 400	5.4	28.4	19	10	DV748318	DV748318	ID0AAH12C	C 473	5.4	28.4	19	11	A2855545	A2855545	2M0159P09
C 401	5.4	28.4	19	11	AZ307462	AZ307462	IM0009108	C 474	5.4	28.4	19	11	A2858446	A2858446	2M0163P08
C 402	5.4	28.4	19	11	AZ309043	AZ309043	IM0012008	C 475	5.4	28.4	19	11	A2941399	A2941399	2M0201P07
C 403	5.4	28.4	19	11	AZ309874	AZ309874	IM0017C14	C 476	5.4	28.4	19	11	A2941765	A2941765	2M0201G11
C 404	5.4	28.4	19	11	AZ314143	AZ314143	IM0030K16	C 477	5.4	28.4	19	11	A2977338	A2977338	2M0253P10
C 405	5.4	28.4	19	11	AZ328533	AZ328533	IM0052B19	C 478	5.4	28.4	19	11	A2990856	A2990856	2M0274P14
C 406	5.4	28.4	19	11	AZ330744	AZ330744	IM0056107	C 479	5.4	28.4	19	11	A2991531	A2991531	2M0275K15
C 407	5.4	28.4	19	11	AZ338061	AZ338061	IM0069B05	C 480	5.4	28.4	19	13	CL656067	CL656067	PR10125C
C 408	5.4	28.4	19	11	AZ345593	AZ345593	IM0080E23	C 481	5.4	28.4	19	13	CL657902	CL657902	PR10126_D
C 409	5.4	28.4	19	11	AZ345594	AZ345594	IM0080C23	C 482	5.4	28.4	19	13	CL658001	CL658001	PR10130a
C 410	5.4	28.4	19	11	AZ366147	AZ366147	IM0115D20	C 483	5.4	28.4	19	13	CL668704	CL668704	PR10158b
C 411	5.4	28.4	19	11	AZ371078	AZ371078	IM0122A04	C 484	5.4	28.4	19	13	CL668704	CL668704	PR10158b
C 412	5.4	28.4	19	11	AZ392246	AZ392246	IM0154G12	C 485	5.4	28.4	19	13	CL668834	CL668834	PR10158d
C 413	5.4	28.4	19	11	AZ392507	AZ392507	IM0155H11	C 486	5.4	28.4	19	13	CL680274	CL680274	PR10128C
C 414	5.4	28.4	19	11	AZ393531	AZ393531	IM0155P17	C 487	5.4	28.4	19	13	CL680486	CL680486	PR10129b
C 415	5.4	28.4	19	11	AZ424532	AZ424532	IM0204L07	C 488	5.4	28.4	19	13	CL681299	CL681299	PR10130d
C 416	5.4	28.4	19	11	AZ424757	AZ424757	IM0204G02	C 489	5.4	28.4	19	13	CL693868	CL693868	PR10162d
C 417	5.4	28.4	19	11	AZ428450	AZ428450	IM0210O24	C 490	5.4	28.4	19	14	DU779955	ASXB2967	
C 418	5.4	28.4	19	11	AZ430028	AZ430028	IM0214L16	C 491	5.4	28.4	19	14	DX068083	DX068083	KB-B076L0
C 419	5.4	28.4	19	11	AZ438791	AZ438791	IM0229K01	C 492	5.4	28.4	19	14	DX069382	KB-B078G1	
C 420	5.4	28.4	19	11	AZ440106	AZ440106	IM0231G04	C 493	5.4	28.4	19	14	AJ588343	AJ588343	ArabiIdops
C 421	5.4	28.4	19	11	AZ441752	AZ441752	IM0234K06	C 494	5.4	28.4	19	14	AJ600584	AJ600584	ArabiIdops
C 422	5.4	28.4	19	11	AZ458823	AZ458823	IM0276D07	C 495	5.4	28.4	19	14	ATH525946	ATH525946	ArabiIdops
C 423	5.4	28.4	19	11	AZ478277	AZ478277	IM0298B16	C 496	5.4	28.4	19	14	ATH526841	ArabiIdops	
C 424	5.4	28.4	19	11	AZ480102	AZ480102	IM0301A20	C 497	5.4	28.4	19	14	ATH527280	ArabiIdops	
C 425	5.4	28.4	19	11	AZ480342	AZ480342	IM0301J16	C 498	5.4	28.4	19	14	ATH529702	ArabiIdops	
C 426	5.4	28.4	19	11	AZ485264	AZ485264	IM0312O02	C 500	5.4	28.4	19	14	ATH529725	ArabiIdops	
C 427	5.4	28.4	19	11	AZ488234	AZ488234	IM0318G34	C 501	5.4	28.4	19	14	ATH529954	ArabiIdops	
C 428	5.4	28.4	19	11	AZ491206	AZ491206	IM0324P07	C 502	5.2	27.4	19	14	ATH531977	ArabiIdops	
C 429	5.4	28.4	19	11	AZ496805	AZ496805	IM0333G22	C 503	5.2	27.4	19	1	AA912825	AA912825	o143d11.s
C 430	5.4	28.4	19	11	AZ501453	AZ501453	IM0340M13	C 504	5.2	27.4	19	1	AA977115	AA977115	oq24c08.s
C 431	5.4	28.4	19	11	AZ508288	AZ508288	IM0350A01	C 505	5.2	27.4	19	1	AI160784	AI160784	qx98g07.x
C 432	5.4	28.4	19	11	AZ508487	AZ508487	IM0350H24	C 506	5.2	27.4	19	1	AI583857	AI583857	tc73g05.x
C 433	5.4	28.4	19	11	AZ514386	AZ514386	IM0361H02	C 507	5.2	27.4	19	1	AI918188	AI918188	tn08c09.x
C 434	5.4	28.4	19	11	AZ586377	AZ586377	IM03962A15	C 508	5.2	27.4	19	1	AJ688828	AJ688828	
C 435	5.4	28.4	19	11	AZ588035	AZ588035	IM0396G17	C 509	5.2	27.4	19	1	AM075294	AM075294	
C 436	5.4	28.4	19	11	AZ596312	AZ596312	IM0409D04	C 510	5.2	27.4	19	2	BM936129	BM936129	5009-0-17
C 437	5.4	28.4	19	11	AZ600709	AZ600709	IM0418H10	C 511	5.2	27.4	19	4	BK550886	BK550886	
C 438	5.4	28.4	19	11	AZ600896	AZ600896	IM0418J24	C 512	5.2	27.4	19	4	BK554211	BK554211	
C 439	5.4	28.4	19	11	AZ603744	AZ603744	IM0423B15	C 513	5.2	27.4	19	4	BK558720	BK558720	
C 440	5.4	28.4	19	11	AZ623310	AZ623310	IM0460G19	C 514	5.2	27.4	19	4	BK558720	BK558720	
C 441	5.4	28.4	19	11	AZ651803	AZ651803	IM0522N11	C 515	5.2	27.4	19	4	BK560068	BK560068	
C 442	5.4	28.4	19	11	AZ655467	AZ655467	IM0530O17	C 516	5.2	27.4	19	4	BK560254	BK560254	
C 443	5.4	28.4	19	11	AZ660552	AZ660552	IM0538O08	C 517	5.2	27.4	19	4	BK563913	BK563913	
C 444	5.4	28.4	19	11	AZ663032	AZ663032	IM0542M22	C 518	5.2	27.4	19	4	BK563927	BK563927	
C 445	5.4	28.4	19	11	AZ663240	AZ663240	IM0542H18	C 519	5.2	27.4	19	4	BK564633	BK564633	
C 446	5.4	28.4	19	11	AZ663498	AZ663498	IM0543T08	C 520	5.2	27.4	19	4	BK567491	BK567491	
C 447	5.4	28.4	19	11	AZ675967	AZ675967	IM0552I23	C 521	5.2	27.4	19	4	BK568381	BK568381	
C 448	5.4	28.4	19	11	AZ760695	AZ760695	IM0554C07	C 522	5.2	27.4	19	4	BK568469	BK568469	
C 449	5.4	28.4	19	11	AZ768918	AZ768918	IM0569P08	C 523	5.2	27.4	19	4	BK568737	BK568737	
C 450	5.4	28.4	19	11	AZ770542	AZ770542	IM0572K11	C 524	5.2	27.4	19	4	CO0981	CO0981	
C 451	5.4	28.4	19	11	AZ772336	AZ772336	IM0574K14	C 525	5.2	27.4	19	4	CA587421	CA587421	
C 452	5.4	28.4	19	11	AZ772366	AZ772366	IM0583J05	C 526	5.2	27.4	19	4	CA587421	CA587421	
C 453	5.4	28.4	19	11	AZ774950	AZ774950	2M0004K16	C 527	5.2	27.4	19	5	CF298245	CF298245	
C 454	5.4	28.4	19	11	AZ776733	AZ776733	2M0010E07	C 528	5.2	27.4	19	5	CF306225	CF306225	
C 455	5.4	28.4	19	11				C 529	5.2	27.4	19	5	CF312203	ABF--07-M	
C 457	5.4	28.4	19	11				C 530	5.2	27.4	19	5			

531	5.2	27.4	19	5	CF318426	CF318426 HD--08-12	C 604	5.2	27.4	19	11	AZ664297	AZ664297 2M0173L18
532	5.2	27.4	19	7	AM059909	AM059909 AHUTH_bas	C 605	5.2	27.4	19	11	AZ668070	AZ668070 2M0179I07
533	5.2	27.4	19	8	CO778963	CO778963 BL005B_B0	C 606	5.2	27.4	19	11	AZ9347956	AZ9347956 2M0196I08
534	5.2	27.4	19	8	CO779910	CO779910 BL008A_G0	C 607	5.2	27.4	19	11	AZ944615	AZ944615 2M0205H12
535	5.2	27.4	19	8	CO781979	CO781979 BL013D_F1	C 608	5.2	27.4	19	11	AZ991573	AZ991573 2M0275D23
536	5.2	27.4	19	8	CO790444	CO790444 NT009C_G1	C 609	5.2	27.4	19	13	CL873643	CL873643 abe89d05.
537	5.2	27.4	19	8	CO793357	CO793357 NT017C_D0	C 610	5.2	27.4	19	14	AJ587161	AJ587161 ArabiIdops
538	5.2	27.4	19	9	DN161077	DN161077 est a.D1a	C 611	5.2	27.4	19	14	AJ587166	AJ587166 ArabiIdops
539	5.2	27.4	19	9	DN955544	DN955544 it83c1.g	C 612	5.2	27.4	19	14	AJ587167	AJ587167 ArabiIdops
540	5.2	27.4	19	9	DN985675	DN985675 MSU_2F_-2-	C 613	5.2	27.4	19	14	AJ587961	AJ587961 ArabiIdops
541	5.2	27.4	19	9	DR107492	DR107492 JHU140E12	C 614	5.2	27.4	19	14	AJ592461	AJ592461 ArabiIdops
542	5.2	27.4	19	11	AZ309914	AZ309914 IM0017P18	C 615	5.2	27.4	19	14	AJ594463	AJ594463 ArabiIdops
543	5.2	27.4	19	11	AZ316568	AZ316568 IM0034G14	C 616	5.2	27.4	19	14	AJ597470	AJ597470 ArabiIdops
544	5.2	27.4	19	11	AZ322583	AZ322583 IM0043A10	C 617	5.2	27.4	19	14	ATH525440	ATH525440 ArabiIdops
545	5.2	27.4	19	11	AZ324945	AZ324945 IM0047C03	C 618	5.2	27.4	19	14	ATH527642	ATH527642 ArabiIdops
546	5.2	27.4	19	11	AZ340577	AZ340577 IM0072H21	C 619	5.2	27.4	19	14	ATH528618	ATH528618 ArabiIdops
547	5.2	27.4	19	11	AZ342681	AZ342681 IM0075B23	C 620	5.2	27.4	19	14	ATH531443	ATH531443 ArabiIdops
548	5.2	27.4	19	11	AZ343388	AZ343388 IM0076J23	C 621	5.2	27.4	19	14	AA909236	AA909236 ox02d04.8
549	5.2	27.4	19	11	AZ345852	AZ345852 IM0080E18	C 622	5.2	27.4	19	14	AI033338	AI033338 ox02d04.8
550	5.2	27.4	19	11	AZ355195	AZ355195 IM0094G22	C 623	5.2	27.4	19	14	AI077581	AI077581 ox02d04.8
551	5.2	27.4	19	11	AZ361569	AZ361569 IM0106N21	C 624	5.2	27.4	19	14	AI187072	AI187072 qe38a01.8
552	5.2	27.4	19	11	AZ379786	AZ379786 IM0135K09	C 625	5.2	27.4	19	14	AI187072	AI187072 qe38a01.8
553	5.2	27.4	19	11	AZ389577	AZ389577 IM0150I20	C 626	5.2	27.4	19	14	AI1524591	AI1524591 co43f09.x
554	5.2	27.4	19	11	AZ403969	AZ403969 IM0172B03	C 627	5.2	27.4	19	14	AI570374	AI570374 co78f07.x
555	5.2	27.4	19	11	AZ406101	AZ406101 IM0175O11	C 628	5.2	27.4	19	14	AI625518	AI625518 lvs6d06.x
556	5.2	27.4	19	11	AZ427411	AZ427411 IM0209A22	C 629	5.2	27.4	19	14	AI648553	AI648553 lvs5e07.x
557	5.2	27.4	19	11	AZ437653	AZ437653 IM0209B14	C 630	5.2	27.4	19	14	AI678558	AI678558 lvs3h07.x
558	5.2	27.4	19	11	AZ441188	AZ441188 IM0232004	C 631	5.2	27.4	19	14	AI678558	AI678558 lvs3h07.x
559	5.2	27.4	19	11	AZ457710	AZ457710 IM0261K07	C 632	5.2	27.4	19	14	AI678558	AI678558 lvs3h07.x
560	5.2	27.4	19	11	AZ465883	AZ465883 IM0276D07	C 633	5.2	27.4	19	14	AI6550046	AI6550046 AJ650046
561	5.2	27.4	19	11	AZ466725	AZ466725 IM0277C09	C 634	5.2	27.4	19	14	AI6550046	AI6550046 AJ650046
562	5.2	27.4	19	11	AZ475079	AZ475079 IM0293B17	C 635	5.2	27.4	19	14	AI662060	AI662060 AJ662060
563	5.2	27.4	19	11	AZ480102	AZ480102 IM0301A20	C 636	5.2	27.4	19	14	AI666241	AI666241 AJ666241
564	5.2	27.4	19	11	AZ490111	AZ490111 IM0322H17	C 637	5.2	27.4	19	14	AI671616	AI671616 AJ671616
565	5.2	27.4	19	11	AZ490549	AZ490549 IM0323N03	C 638	5.2	27.4	19	14	AI672970	AI672970 AJ672970
566	5.2	27.4	19	11	AZ510138	AZ510138 IM0354O21	C 639	5.2	27.4	19	14	AI746804	AI746804 AJ746804
567	5.2	27.4	19	11	AZ514467	AZ514467 IM0361B19	C 640	5.2	27.4	19	14	AL037236	AL037236 DKP2564L
568	5.2	27.4	19	11	AZ579954	AZ579954 IM0368C02	C 641	5.2	27.4	19	14	BM075343	BM075343 ANO75343
569	5.2	27.4	19	11	AZ581163	AZ581163 IM0369M20	C 642	5.2	27.4	19	14	BM3927923	BM3927923 HNC45-1-E
570	5.2	27.4	19	11	AZ585898	AZ585898 IM0391L22	C 643	5.2	27.4	19	14	BM394390	BM394390 50072-2-3
571	5.2	27.4	19	11	AZ589109	AZ589109 IM0397D22	C 644	5.2	27.4	19	14	BM397569	BM397569 50072-2-7
572	5.2	27.4	19	11	AZ591963	AZ591963 IM0402P23	C 645	5.2	27.4	19	14	BM397569	BM397569 5009-0-34
573	5.2	27.4	19	11	AZ601003	AZ601003 IM0419M06	C 646	5.2	27.4	19	14	BM399311	BM399311 5009-0-56
574	5.2	27.4	19	11	AZ622447	AZ622447 IM0459I15	C 647	5.2	27.4	19	14	BM399863	BM399863 5009-0-62
575	5.2	27.4	19	11	AZ623785	AZ623785 IM0461P16	C 648	5.2	27.4	19	14	BM400740	BM400740 5009-0-78
576	5.2	27.4	19	11	AZ636812	AZ636812 IM0495B21	C 649	5.2	27.4	19	14	BQ789814	BQ789814 h8ge002aF
577	5.2	27.4	19	11	AZ644418	AZ644418 IM0508B20	C 650	5.2	27.4	19	14	BX548528	BX548528 BX548528
578	5.2	27.4	19	11	AZ645469	AZ645469 IM0510L24	C 651	5.2	27.4	19	14	BX551805	BX551805 BX551805
579	5.2	27.4	19	11	AZ645469	AZ645469 IM0510L24	C 652	5.2	27.4	19	14	CA0646	CA0646 HUM6S000819
580	5.2	27.4	19	11	AZ648801	AZ648801 IM0518A10	C 653	5.2	27.4	19	14	CA587421	CA587421 LBE12P23
581	5.2	27.4	19	11	AZ655972	AZ655972 IM0531C16	C 654	5.2	27.4	19	14	CB412539	CB412539 SCAE_0892
582	5.2	27.4	19	11	AZ656937	AZ656937 IM0532K13	C 655	5.2	27.4	19	14	CB412539	CB412539 SCAE_0892
583	5.2	27.4	19	11	AZ657685	AZ657685 IM0534I06	C 656	5.2	27.4	19	14	CB413855	CB413855 SCAE_2576
584	5.2	27.4	19	11	AZ659603	AZ659603 IM0537N06	C 657	5.2	27.4	19	14	CB415466	CB415466 SCAE_4656
585	5.2	27.4	19	11	AZ662546	AZ662546 IM0541P08	C 658	5.2	27.4	19	14	CD533793	CD533793 3312J_Ara
586	5.2	27.4	19	11	AZ663498	AZ663498 IM0543I08	C 659	5.2	27.4	19	14	CF296463	CF296463 30DGS--06
587	5.2	27.4	19	11	AZ665203	AZ665203 IM0546B05	C 660	5.2	27.4	19	14	CF298887	CF298887 7LEAF--02
588	5.2	27.4	19	11	AZ759898	AZ759898 IM0553A08	C 661	5.2	27.4	19	14	CF298891	CF298891 7LEAF--02
589	5.2	27.4	19	11	AZ763729	AZ763729 IM0559N16	C 662	5.2	27.4	19	14	CF299279	CF299279 7LEAF--03
590	5.2	27.4	19	11	AZ772432	AZ772432 IM0583L17	C 663	5.2	27.4	19	14	CF303019	CF303019 ABF1--01
591	5.2	27.4	19	11	AZ775273	AZ775273 IM06007F04	C 664	5.2	27.4	19	14	CF306449	CF306449 HDA1--03-E
592	5.2	27.4	19	11	AZ775865	AZ775865 IM06009F05	C 665	5.2	27.4	19	14	CF322872	CF322872 HNN--02-E
593	5.2	27.4	19	11	AZ778052	AZ778052 IM0613A01	C 666	5.2	27.4	19	14	CF329137	CF329137 NACL--04-E
594	5.2	27.4	19	11	AZ782828	AZ782828 IM06204H06	C 667	5.2	27.4	19	14	CNS08V82	CNS08V82 Single re
595	5.2	27.4	19	11	AZ785819	AZ785819 IM0630PF04	C 668	5.2	27.4	19	14	CNS09MXK	CNS09MXK Single re
596	5.2	27.4	19	11	AZ787558	AZ787558 IM0634A07	C 669	5.2	27.4	19	14	AM250665	AM250665 2822622.5
597	5.2	27.4	19	11	AZ805995	AZ805995 IM0657P13	C 670	5.2	27.4	19	14	CN498250	CN498250 P04_02622
598	5.2	27.4	19	11	AZ812572	AZ812572 IM0679O15	C 671	5.2	27.4	19	14	CN498250	CN498250 P04_02622
599	5.2	27.4	19	11	AZ814554	AZ814554 IM0682P13	C 672	5.2	27.4	19	14	CO577706	CO577706 TVEST082C
600	5.2	27.4	19	11	AZ818659	AZ818659 IM0688N17	C 673	5.2	27.4	19	14	CO578459	CO578459 TVEST093E
601	5.2	27.4	19	11	AZ825396	AZ825396 IM0100N04	C 674	5.2	27.4	19	14	CO786076	CO786076 BL285B_E0
602	5.2	27.4	19	11	AZ828745	AZ828745 IM0105J19	C 675	5.2	27.4	19	14	CO786107	CO786107 BL285B_H0
603	5.2	27.4	19	11	AZ839642	AZ839642 IM0135C23	C 676	5.2	27.4	19	14	CV933279	CV933279 pwpcm_050

677	5	26.3	19	8	CX000508	CX000508	lv58b09.g	750	5	26.3	19	11	AZ808212	AZ808212	2M0071D03
678	5	26.3	19	8	CX001762	CX001762	lv42h09.b	751	5	26.3	19	11	AZ811036	AZ811036	2M0077B05
679	5	26.3	19	9	DN955504	DN955504	lt88g06.g	752	5	26.3	19	11	AZ813099	AZ813099	2M0080B09
680	5	26.3	19	9	DN955507	DN955507	lt88g10.g	753	5	26.3	19	11	AZ814554	AZ814554	2M0082P13
681	5	26.3	19	9	DR107492	DR107492	ltHUI40E12	754	5	26.3	19	11	AZ818421	AZ818421	2M0088M19
682	5	26.3	19	9	DR107588	DR107588	ltHUI42G08	755	5	26.3	19	11	AZ819775	AZ819775	2M0091D01
683	5	26.3	19	10	DV671674	DV671674	Col-B12 A	756	5	26.3	19	11	AZ822457	AZ822457	2M0095D16
684	5	26.3	19	11	AQ990183	AQ990183	RfC00908	757	5	26.3	19	11	AZ826361	AZ826361	2M0102H04
685	5	26.3	19	11	AZ303949	AZ303949	IM0003M19	758	5	26.3	19	11	AZ827840	AZ827840	2M0104F01
686	5	26.3	19	11	AZ309643	AZ309643	IM0016E23	759	5	26.3	19	11	AZ829723	AZ829723	2M0107I22
687	5	26.3	19	11	AZ313113	AZ313113	IM0029M17	760	5	26.3	19	11	AZ831190	AZ831190	2M0110K18
688	5	26.3	19	11	AZ314770	AZ314770	IM0031B16	761	5	26.3	19	11	AZ834005	AZ834005	2M0116P20
689	5	26.3	19	11	AZ319924	AZ319924	IM0039C15	762	5	26.3	19	11	AZ834875	AZ834875	2M0117L13
690	5	26.3	19	11	AZ327390	AZ327390	IM0050L09	763	5	26.3	19	11	AZ835621	AZ835621	2M0129L21
691	5	26.3	19	11	AZ331082	AZ331082	IM0056C13	764	5	26.3	19	11	AZ839043	AZ839043	2M0135D04
692	5	26.3	19	11	AZ335137	AZ335137	IM0064P16	765	5	26.3	19	11	AZ842496	AZ842496	2M0141D04
693	5	26.3	19	11	AZ339847	AZ339847	IM0071C06	766	5	26.3	19	11	AZ848978	AZ848978	2M0164P24
694	5	26.3	19	11	AZ345964	AZ345964	IM0081D01	767	5	26.3	19	11	AZ864551	AZ864551	2M0174M11
695	5	26.3	19	11	AZ345964	AZ345964	IM0081D01	768	5	26.3	19	11	AZ868818	AZ868818	2M0180L11
696	5	26.3	19	11	AZ358656	AZ358656	IM0101K12	769	5	26.3	19	11	AZ871037	AZ871037	2M0183C16
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698	5	26.3	19	11	AZ370656	AZ370656	IM0121P18	771	5	26.3	19	11	AZ954985	AZ954985	2M0220H21
699	5	26.3	19	11	AZ394490	AZ394490	IM0158D05	772	5	26.3	19	11	AZ994163	AZ994163	2M0279P05
700	5	26.3	19	11	AZ397615	AZ397615	IM0162M07	773	5	26.3	19	11	CH541244	CH541244	HPYCH41V-
701	5	26.3	19	11	AZ414372	AZ414372	IM0186G18	774	5	26.3	19	13	C283815	C283815	CP31h12.f
702	5	26.3	19	11	AZ422762	AZ422762	IM0201P12	775	5	26.3	19	13	CL670097	CL670097	PR10161a
703	5	26.3	19	11	AZ426675	AZ426675	IM0206N21	776	5	26.3	19	13	CL671134	CL671134	PR10163d
704	5	26.3	19	11	AZ442378	AZ442378	IM0236K18	777	5	26.3	19	13	CL671780	CL671780	PR10165c
705	5	26.3	19	11	AZ442391	AZ442391	IM0236P13	778	5	26.3	19	13	CL687732	CL687732	PR10147c
706	5	26.3	19	11	AZ445457	AZ445457	IM0241J13	779	5	26.3	19	14	AJ587169	AJ587169	Arb1d0ps
707	5	26.3	19	11	AZ447652	AZ447652	IM0244M24	780	5	26.3	19	14	AJ588791	AJ588791	Arb1d0ps
708	5	26.3	19	11	AZ465132	AZ465132	IM0274D24	781	5	26.3	19	14	AJ590235	AJ590235	Arb1d0ps
709	5	26.3	19	11	AZ477353	AZ477353	IM0296K16	782	5	26.3	19	14	AJ594370	AJ594370	Arb1d0ps
710	5	26.3	19	11	AZ477353	AZ477353	IM0296K16	783	5	26.3	19	14	AJ595406	AJ595406	Arb1d0ps
711	5	26.3	19	11	AZ478491	AZ478491	IM0298P03	784	5	26.3	19	14	AJ598867	AJ598867	Arb1d0ps
712	5	26.3	19	11	AZ480113	AZ480113	IM0301F20	785	5	26.3	19	14	ATH525591	ATH525591	Arb1d0ps
713	5	26.3	19	11	AZ480342	AZ480342	IM0301J16	786	5	26.3	19	14	ATH529281	ATH529281	Arb1d0ps
714	5	26.3	19	11	AZ480982	AZ480982	IM0302I14	787	5	26.3	19	14	ATH529363	ATH529363	Arb1d0ps
715	5	26.3	19	11	AZ481449	AZ481449	IM0303N07	788	5	26.3	19	14	TA308010	TA308010	Arb1d0ps
716	5	26.3	19	11	AZ484303	AZ484303	IM0310K12	789	4.8	25.3	19	1	AA884867	AA884867	am21b11.s
717	5	26.3	19	11	AZ490612	AZ490612	IM0323L11	790	4.8	25.3	19	1	AA928040	AA928040	o158g09.s
718	5	26.3	19	11	AZ493714	AZ493714	IM0328T04	791	4.8	25.3	19	1	AJ027323	AJ027323	ow46a07.s
719	5	26.3	19	11	AZ494890	AZ494890	IM0330N19	792	4.8	25.3	19	1	AJ049374	AJ049374	ub33a03.x
720	5	26.3	19	11	AZ498063	AZ498063	IM0335J08	793	4.8	25.3	19	1	AJ1360784	AJ1360784	qx98g07.x
721	5	26.3	19	11	AZ579189	AZ579189	IM0363I12	794	4.8	25.3	19	1	AJ1538541	AJ1538541	td08a11.x
722	5	26.3	19	11	AZ585367	AZ585367	IM0390D06	795	4.8	25.3	19	1	AJ1538541	AJ1538541	td08a11.x
723	5	26.3	19	11	AZ586043	AZ586043	IM0391L12	796	4.8	25.3	19	1	AJ1584018	AJ1584018	ts12e10.x
724	5	26.3	19	11	AZ586752	AZ586752	IM0392M24	797	4.8	25.3	19	1	AJ1804310	AJ1804310	tc65g08.x
725	5	26.3	19	11	AZ595885	AZ595885	IM0408L15	798	4.8	25.3	19	1	AJ647163	AJ647163	AJ647163
726	5	26.3	19	11	AZ597767	AZ597767	IM0411C22	799	4.8	25.3	19	1	AJ649246	AJ649246	AJ649246
727	5	26.3	19	11	AZ613058	AZ613058	IM0441C18	800	4.8	25.3	19	1	AJ650841	AJ650841	AJ650841
728	5	26.3	19	11	AZ621656	AZ621656	IM0455C01	801	4.8	25.3	19	1	AJ657561	AJ657561	AJ657561
729	5	26.3	19	11	AZ623493	AZ623493	IM0461M13	802	4.8	25.3	19	1	AJ657936	AJ657936	AJ657936
730	5	26.3	19	11	AZ626685	AZ626685	IM0467M01	803	4.8	25.3	19	1	AJ660078	AJ660078	AJ660078
731	5	26.3	19	11	AZ630503	AZ630503	IM0484O20	804	4.8	25.3	19	1	AJ663392	AJ663392	AJ663392
732	5	26.3	19	11	AZ639833	AZ639833	IM0501H05	805	4.8	25.3	19	1	AJ747293	AJ747293	AJ747293
733	5	26.3	19	11	AZ643124	AZ643124	IM0506P02	806	4.8	25.3	19	1	AM075423	AM075423	AM075423
734	5	26.3	19	11	AZ654214	AZ654214	IM0528H13	807	4.8	25.3	19	1	AM075491	AM075491	AM075491
735	5	26.3	19	11	AZ656517	AZ656517	IM0532P04	808	4.8	25.3	19	1	AM075504	AM075504	AM075504
736	5	26.3	19	11	AZ658282	AZ658282	IM0535C02	809	4.8	25.3	19	1	AJ013837	AJ013837	AJ013837
737	5	26.3	19	11	AZ659191	AZ659191	IM0536J19	810	4.8	25.3	19	2	BM395626	BM395626	BM395626
738	5	26.3	19	11	AZ661787	AZ661787	IM0540I06	811	4.8	25.3	19	2	BM395679	BM395679	BM395679
739	5	26.3	19	11	AZ675944	AZ675944	IM0553O10	812	4.8	25.3	19	2	BM395733	BM395733	BM395733
740	5	26.3	19	11	AZ772136	AZ772136	IM0574K14	813	4.8	25.3	19	2	BM395769	BM395769	BM395769
741	5	26.3	19	11	AZ772446	AZ772446	IM0583O16	814	4.8	25.3	19	2	BM395792	BM395792	BM395792
742	5	26.3	19	11	AZ774477	AZ774477	2M0004A03	815	4.8	25.3	19	2	BM395830	BM395830	BM395830
743	5	26.3	19	11	AZ787654	AZ787654	2M0023D08	816	4.8	25.3	19	2	BM396147	BM396147	BM396147
744	5	26.3	19	11	AZ787654	AZ787654	2M0034B16	817	4.8	25.3	19	2	BM396288	BM396288	BM396288
745	5	26.3	19	11	AZ789771	AZ789771	2M0037D24	818	4.8	25.3	19	2	BM396403	BM396403	BM396403
746	5	26.3	19	11	AZ789827	AZ789827	2M0038C02	819	4.8	25.3	19	2	BM396507	BM396507	BM396507
747	5	26.3	19	11	AZ794653	AZ794653	2M0048G05	820	4.8	25.3	19	2	BM396664	BM396664	BM396664
748	5	26.3	19	11	AZ799057	AZ799057	2M0056B20	821	4.8	25.3	19	2	BM397535	BM397535	BM397535
749	5	26.3	19	11	AZ803930	AZ803930	2M0064N01	822	4.8	25.3	19	2	BM397535	BM397535	BM397535

823	4.8	25.3	19	2	BM397569	BM397569	5009-0-34	896	4.8	25.3	19	11	AZ357958	AZ357958	1M0039D23
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825	4.8	25.3	19	2	BM397697	BM397697	5009-0-35	898	4.8	25.3	19	11	AZ358825	AZ358825	1M0101J20
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829	4.8	25.3	19	2	BM398182	BM398182	5009-0-41	902	4.8	25.3	19	11	AZ400662	AZ400662	1M0167K06
830	4.8	25.3	19	2	BM398405	BM398405	5009-0-45	903	4.8	25.3	19	11	AZ410350	AZ410350	1M0162D09
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833	4.8	25.3	19	2	BM398524	BM398524	5009-0-46	906	4.8	25.3	19	11	AZ427754	AZ427754	1M0209N23
834	4.8	25.3	19	2	BM398776	BM398776	5009-0-50	907	4.8	25.3	19	11	AZ434551	AZ434551	1M0221C12
835	4.8	25.3	19	2	BM398878	BM398878	5009-0-50	908	4.8	25.3	19	11	AZ435252	AZ435252	1M0222D11
836	4.8	25.3	19	2	BM398882	BM398882	5009-0-50	909	4.8	25.3	19	11	AZ442257	AZ442257	1M0234L23
837	4.8	25.3	19	2	BM398909	BM398909	5009-0-56	910	4.8	25.3	19	11	AZ442351	AZ442351	1M0236P13
838	4.8	25.3	19	2	BM399105	BM399105	5009-0-53	911	4.8	25.3	19	11	AZ4475705	AZ4475705	1M0294B02
839	4.8	25.3	19	2	BM399219	BM399219	5009-0-55	912	4.8	25.3	19	11	AZ480292	AZ480292	1M0301M09
840	4.8	25.3	19	2	BM399274	BM399274	5009-0-56	913	4.8	25.3	19	11	AZ480292	AZ480292	1M0301M09
841	4.8	25.3	19	2	BM399311	BM399311	5009-0-56	914	4.8	25.3	19	11	AZ480905	AZ480905	1M0302N22
842	4.8	25.3	19	2	BM399311	BM399311	5009-0-56	915	4.8	25.3	19	11	AZ481973	AZ481973	1M0306J12
843	4.8	25.3	19	2	BM399684	BM399684	5009-0-60	916	4.8	25.3	19	11	AZ482658	AZ482658	1M0307L16
844	4.8	25.3	19	2	BM399763	BM399763	5009-0-61	917	4.8	25.3	19	11	AZ485378	AZ485378	1M0312F16
845	4.8	25.3	19	2	BM399791	BM399791	5009-0-61	918	4.8	25.3	19	11	AZ489548	AZ489548	1M0322L05
846	4.8	25.3	19	2	BM399859	BM399859	5009-0-62	919	4.8	25.3	19	11	AZ490506	AZ490506	1M0323E06
847	4.8	25.3	19	2	BM400013	BM400013	5009-0-64	920	4.8	25.3	19	11	AZ496535	AZ496535	1M0333F04
848	4.8	25.3	19	2	BM400383	BM400383	5009-0-72	921	4.8	25.3	19	11	AZ500630	AZ500630	1M0339A10
849	4.8	25.3	19	2	BM400545	BM400545	5009-0-75	922	4.8	25.3	19	11	AZ508355	AZ508355	1M0350O13
850	4.8	25.3	19	2	BM400545	BM400545	5009-0-75	923	4.8	25.3	19	11	AZ508519	AZ508519	1M0350O21
851	4.8	25.3	19	2	BM400925	BM400925	5009-0-80	924	4.8	25.3	19	11	AZ509071	AZ509071	1M0351A21
852	4.8	25.3	19	2	BM400987	BM400987	5009-0-81	925	4.8	25.3	19	11	AZ514533	AZ514533	1M0361H08
853	4.8	25.3	19	2	BM401020	BM401020	5009-0-81	926	4.8	25.3	19	11	AZ514573	AZ514573	1M0361J12
854	4.8	25.3	19	2	BM401035	BM401035	5009-0-81	927	4.8	25.3	19	11	AZ514586	AZ514586	1M0361P07
855	4.8	25.3	19	2	BM401080	BM401080	5009-0-82	928	4.8	25.3	19	11	AZ514792	AZ514792	1M0361B17
856	4.8	25.3	19	2	BM401080	BM401080	5009-0-82	929	4.8	25.3	19	11	AZ517931	AZ517931	1M0363P12
857	4.8	25.3	19	2	BM401163	BM401163	5009-0-83	930	4.8	25.3	19	11	AZ525811	AZ525811	1M0369N08
858	4.8	25.3	19	2	BM401213	BM401213	5009-0-84	931	4.8	25.3	19	11	AZ528215	AZ528215	1M0374C19
859	4.8	25.3	19	2	BM401275	BM401275	5009-0-85	932	4.8	25.3	19	11	AZ5288035	AZ5288035	1M0396G17
860	4.8	25.3	19	2	BM401359	BM401359	5009-0-85	933	4.8	25.3	19	11	AZ5288918	AZ5288918	1M0397J05
861	4.8	25.3	19	4	BX552609	BX552609	5009-0-9-	934	4.8	25.3	19	11	AZ5589162	AZ5589162	1M0397O23
862	4.8	25.3	19	4	CO1216	CO1216	HOMG5000792	935	4.8	25.3	19	11	AZ565570	AZ565570	1M0408I15
863	4.8	25.3	19	4	CO1993	CO1993	HOMG5000792	936	4.8	25.3	19	11	AZ565570	AZ565570	1M0408I15
864	4.8	25.3	19	4	CB415418	CB415418	SCAE 4589	937	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
865	4.8	25.3	19	5	CF303019	CF303019	ABF1--01-	938	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
866	4.8	25.3	19	5	CF306449	CF306449	HDA1--03-	939	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
867	4.8	25.3	19	5	CF307006	CF307006	HDA1--05-	940	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
868	4.8	25.3	19	5	CF307304	CF307304	HDA1--06-	941	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
869	4.8	25.3	19	5	CF307439	CF307439	ABF--06-	942	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
870	4.8	25.3	19	5	CF311635	CF311635	ABF--06-	943	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
871	4.8	25.3	19	5	CF334260	CF334260	JMT--03-H	944	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
872	4.8	25.3	19	7	AM247975	AM247975	2820669.3	945	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
873	4.8	25.3	19	8	CN750859	CN750859	ADPT-KXVI	946	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
874	4.8	25.3	19	8	CO780477	CO780477	BL009D_A0	947	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
875	4.8	25.3	19	8	CO780622	CO780622	BL010A_F0	948	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
876	4.8	25.3	19	8	CO783138	CO783138	BL017A_G0	949	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
877	4.8	25.3	19	8	CO783722	CO783722	BL018D_B0	950	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
878	4.8	25.3	19	8	CO786107	CO786107	BL2858_H0	951	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
879	4.8	25.3	19	8	CO786107	CO786107	BL2858_H0	952	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
880	4.8	25.3	19	8	CO786107	CO786107	BL2858_H0	953	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
881	4.8	25.3	19	9	D17097	D17097	MSU 2R 2-	954	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
882	4.8	25.3	19	9	DM986391	DM986391	MSU 2R 2-	955	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
883	4.8	25.3	19	11	DR065340	DR065340	1P93411-G	956	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
884	4.8	25.3	19	11	AZ308423	AZ308423	1M0011E21	957	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
885	4.8	25.3	19	11	AZ309043	AZ309043	1M0012C08	958	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
886	4.8	25.3	19	11	AZ309531	AZ309531	1M0013K06	959	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
887	4.8	25.3	19	11	AZ313531	AZ313531	1M0029N07	960	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
888	4.8	25.3	19	11	AZ317359	AZ317359	1M0036J02	961	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
889	4.8	25.3	19	11	AZ318731	AZ318731	1M0038G08	962	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
890	4.8	25.3	19	11	AZ329936	AZ329936	1M0054L10	963	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
891	4.8	25.3	19	11	AZ336303	AZ336303	1M0065G03	964	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
892	4.8	25.3	19	11	AZ338684	AZ338684	1M0069A24	965	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
893	4.8	25.3	19	11	AZ340126	AZ340126	1M0072A23	966	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
894	4.8	25.3	19	11	AZ342555	AZ342555	1M0075K11	967	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
895	4.8	25.3	19	11	AZ345359	AZ345359	1M0079D23	968	4.8	25.3	19	11	AZ565570	AZ565570	1M0428N14
					AZ346703	AZ346703	1M0082L05								

C 969	4.8	25.3	19	11	AZ815067	AZ815067	2M0083P01
C 970	4.8	25.3	19	11	AZ817238	AZ817238	2M0086E01
C 971	4.8	25.3	19	11	AZ819494	AZ819494	2M0091I10
C 972	4.8	25.3	19	11	AZ822457	AZ822457	2M0095D16
C 973	4.8	25.3	19	11	AZ836630	AZ836630	2M0131I05
C 974	4.8	25.3	19	11	AZ849303	AZ849303	2M0150K08
C 975	4.8	25.3	19	11	AZ854718	AZ854718	2M0158N23
C 976	4.8	25.3	19	11	AZ862758	AZ862758	2M0170O05
C 977	4.8	25.3	19	11	AZ864822	AZ864822	2M0174C08
C 978	4.8	25.3	19	11	AZ875430	AZ875430	2M0189K09
C 979	4.8	25.3	19	11	AZ8942806	AZ8942806	2M0203P09
C 980	4.8	25.3	19	11	AZ899188	AZ899188	2M0212I04
C 981	4.8	25.3	19	11	AZ8990039	AZ8990039	2M0213N20
C 982	4.8	25.3	19	11	AZ8962953	AZ8962953	2M0231P19
C 983	4.8	25.3	19	11	AZ8989738	AZ8989738	2M023M10
C 984	4.8	25.3	19	11	AZ8990193	AZ8990193	2M0273L15
C 985	4.8	25.3	19	11	AZ8991606	AZ8991606	2M0275K24
C 986	4.8	25.3	19	11	AZ8991837	AZ8991837	2M0276E17
C 987	4.8	25.3	19	11	BZ425196	BZ425196	100026548
C 988	4.8	25.3	19	11	CZ284286	CZ284286	CP34F06.r
C 989	4.8	25.3	19	13	CL657902	CL657902	PR1012d.D
C 990	4.8	25.3	19	13	CL664078	CL664078	PR10146a
C 991	4.8	25.3	19	13	CL674770	CL674770	PR10113a
C 992	4.8	25.3	19	13	CL680494	CL680494	PR10129b
C 993	4.8	25.3	19	13	CL688118	CL688118	PR10148c
C 994	4.8	25.3	19	14	DU833338	DU833338	KBx501102
C 995	4.8	25.3	19	14	AJ587169	AJ587169	Arabidops
C 996	4.8	25.3	19	14	AJ592567	AJ592567	Arabidops
C 997	4.8	25.3	19	14	AJ592764	AJ592764	Arabidops
C 998	4.8	25.3	19	14	AJ595189	AJ595189	Arabidops
C 999	4.8	25.3	19	14	AJ599121	AJ599121	Arabidops
C1000	4.8	25.3	19	14	AJ600880	AJ600880	Arabidops

ALIGNMENTS

RESULT 1
LOCUS CL671134/c
DEFINITION PRI0163d.H11 - PRI0163d.B21 (19) Note: Recurring String Mixed fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL671134
VERSION CL671134
KEYWORDS GI:50169817
SOURCE GSS.

ORGANISM Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppRAD: an AcedB database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447

COMMENT

Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Classes: fosmid ends.
Location/Qualifiers

FEATURES

source
1..19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"

ORIGIN

Query Match 56.8%; Score 10.8; DB 13; Length 19;
Best Local Similarity 85.7%; Pred. No. 8.4e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

3 CACGGTATCTCCTT 16
19 CACCGTCTCTCCTT 6

Db

RESULT 2

LOCUS AZ481008
DEFINITION 1M0302N15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0302N15 R, genomic survey sequence.

ACCESSION

AZ481008

VERSION

AZ481008

KEYWORDS

AZ481008.1 GI:10641989
GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rettly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niedermauern,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: N column: 15
Seq primer: CACACGGAACACGTATGACC
Classes: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0302N15"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[g14732072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 51.6%; Score 9.8; DB 11; Length 19;
 Best Local Similarity 84.6%; Pred. No. 2.9e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 4 ACGGATTCCTT 16
 |||||
 2 ACGGAGCTGCTT 14
 |||||

Query Match 45.3%; Score 8.6; DB 11; Length 19;
 Best Local Similarity 73.3%; Pred. No. 1.3e+07;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 3 CACGATTCCTTC 17
 |||||
 4 CACCAATCTACTTC 18
 |||||

RESULT 3

AZ309116 19 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0012E23R Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0012E23 R, genomic survey sequence.

RESULT 4
 CF317235 19 bp mRNA linear EST 15-AUG-2003
 LOCUS HD--06-N19.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION AZ309116.1 GI:10349784
 VERSION GSS.
 KEYWORDS Mus musculus (house mouse)
 SOURCE

ACCESSION CF317235.1 GI:33688996
 VERSION CF317235
 KEYWORDS Oryza sativa (japonica cultivar-group)
 SOURCE

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.

ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.

REFERENCE 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0012E23"
 /sex="male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

FEATURES
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 1..19
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 /mol_type="mRNA"
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 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_1lb="OSHDA1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: PCRA-TOP0; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

FEATURES

ORIGIN

Query Match 44.2%; Score 8.4; DB 5; Length 19;
 Best Local Similarity 90.0%; Pred. No. 1.7e+07;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 8 TATCTCCTTC 17
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 10 TATCTCTAC 19
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RESULT 5
 CF929669 19 bp mRNA linear EST 12-NOV-2003
 LOCUS CF929669

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DEFINITION      CF-01-R-E08 Bos taurus CF-24-HW cDNA library Bos taurus cDNA clone
ACCESSION       CF0292669
VERSION         CF0292669.1 GI:38278141
KEYWORDS        EST
SOURCE          Bos taurus (cattle)
ORGANISM        Bos taurus
                Bos taurus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                Pecora; Bovidae; Bovinae; Bos.
REFERENCE       1 (bases 1 to 19)
                Yoon,D.H., Lee,S.H., Lee,J.H., Sang,B.C. and Oh,S.J.
                Gene Expression Profiling of the Bovine adipose tissues
                Unpublished (2003)
JOURNAL         Contact: Dr. Du-Hak Yoon
                National Livestock Research Institute, RDA
                564 Omoekchun-dong, Suwon, 441-350, Korea
                Tel: 82 31 290 1593
                Fax: 82 31 290 1792
                Email: dhyoon@rda.go.kr
                Insert Length: 19 Std Error: 0.00
                Seq primer: ATTAACCTCCTCAAG
                POLYA=No.

FEATURES
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                /sex="Four males mixed"
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                /cell_type="adipocyte"
                /dev_stage="24 months old"
                /lab_host="X11-BlueMRP, strata"
                /clone_11b="Bos taurus CF-24-HW cDNA library"
                /note="Vector: Uni-ZAPXR; Site_1: EcoRI; Site_2: Xho I"

ORIGIN
Query Match      43.2%; Score 8.2; DB 5; Length 19;
Best Local Similarity 76.9%; Pred. No. 2.1e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY              7 GTATCTCCTTCAC 19
                |||||
                7 GGATCTGCATCAC 19

RESULT 6
A0840508        19 bp      DNA      linear      GSS 08-FEB-2006
LOCUS           Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION      594F08 genomic survey sequence.
ACCESSION       AJ840508
VERSION         AJ840508.1 GI:52544714
KEYWORDS        GSS; left border; T-DNA flanking sequence.
SOURCE          Arabidopsis thaliana (thale cress)
ORGANISM        Arabidopsis thaliana
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE       1
                Brnaut,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
                Chauvin,S., Bechtold,N., Crnaud,C., DeRose,R., Pelletier,G.,
                Lepoint,L., Caboche,M. and Lecharny,A.
                T-DNA integration into the Arabidopsis genome depends on sequences
                of pre-insertion sites
                EMBO Rep. 3 (12), 1152-1157 (2002)
JOURNAL         2 (bases 1 to 19)
                Balzerque,S.
                Direct Submision
                Submitted (21-SEP-2004) Balzerque S., UMRGV, INRA/CNRS, 2 rue
                Gaston Cremlieux, 91057 Evry cedex, FRANCE

```

```

COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publicines/. This sequence has
been generated in the framework of the French plant genomics
program 'genoplante' (http://www.genoplante.com and
http://genoplante-info.intobio.gen.fr).

FEATURES
  source        1..19
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /cultivar="Wassiliewskija"
                /db_xref="taxon:3702"
                /clone="594F08"
                /clone_11b="Arabidopsis thaliana T-DNA insertion lines"
                /ecotype="Wassiliewskija"
                /note="T-DNA flanking sequence
                left border"

ORIGIN
Query Match      43.2%; Score 8.2; DB 14; Length 19;
Best Local Similarity 76.9%; Pred. No. 2.1e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY              7 GTATCTCCTTCAC 19
                |||||
                4 GAATCTCCTGAAC 16

RESULT 7
CD532073        19 bp      mRNA      linear      EST 31-DEC-2003
LOCUS           13104 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
DEFINITION      3', mRNA sequence.
ACCESSION       CD532073
VERSION         CD532073.1 GI:40452085
KEYWORDS        EST.
SOURCE          Arabidopsis thaliana
                Arabidopsis thaliana
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE       1 (bases 1 to 19)
                Guo,Y., Cai,Z. and Gan,S.
                Transcriptome of Arabidopsis leaf senescence
                Plant Cell Environ. 27 (5), 521-549 (2004)
JOURNAL         Contact: Shuheng Gan
                Department of Horticulture
                Cornell University
                119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
                Tel: 607 254 5418
                Fax: 607 255 0599
                Email: sg288@cornell.edu
                Insert Length: 19 Std Error: 0.00
                Seq primer: 77
                POLYA=No.

FEATURES
  source        1..19
                /organism="Arabidopsis thaliana"
                /mol_type="mRNA"
                /ecotype="landsberg erecta"
                /db_xref="taxon:3702"
                /tissue_type="leaf"
                /dev_stage="Yellow Leaf With Greenish Base Area"
                /lab_host="E. coli"
                /clone_11b="Arabidopsis leaf Senescence Library"
                /note="Organ: Rosette leaf; Vector: pBluscript SKIT+;
                Site_1: EcoRI; Site_2: EcoRI; Senescent rosette leaves #5

```

and #6 (counted from the bottom) were harvested and immediately frozen in liquid N₂. The leaves were visibly yellow excepted for the leaf base areas that were still greenish."

ORIGIN

Query Match 42.1%; Score 8; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCCTTCAC 19
| | | | |
| | | | |
Db 11 TCCTTCAC 18

RESULT 8

CF280788/c 19 bp mRNA linear EST 14-AUG-2003
LOCUS 14ETL--07-J13.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-J13,
mRNA sequence.

ACCESSION CF280788.1 GI:33658174
VERSION EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

1. 19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--07-J13"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_id="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match 42.1%; Score 8; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CTCCTTCA 18
| | | | |
| | | | |
Db 8 CTCCTTCA 1

RESULT 9

CF299371 19 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-F22.g1 Rice leaf plasmid cDNA library II (7LEAF)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-F22, mRNA
sequence.

ACCESSION CF299371
VERSION CF299371.1 GI:33671132
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

1. 19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-F22"
/issue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_id="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES

1. 19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-F22"
/issue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_id="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match 42.1%; Score 8; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CTCCTTCA 18
| | | | |
| | | | |
Db 18 CTCCTTCA 11

RESULT 10
CF305417/c 19 bp mRNA linear EST 15-AUG-2003
LOCUS CUD1--01-K13.b1 Rice cold treated leaf plasmid cDNA library (CUD1)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone CUD1--01-K13,
mRNA sequence.

ACCESSION CF305417 GI:33677178
VERSION EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

1. 19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-F22"
/issue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_id="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="C1D1--01-K13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library (C1D1)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; Leaf was incubated at 4 C (360um/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

```

ORIGIN

```

Query Match      42.1%; Score 8; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 CTCCTTCA 18
        |||||
        12 CTCCTTCA 5

```

```

RESULT 11
CF315940/c      19 bp      mRNA      linear      EST 15-AUG-2003
LOCUS           HD--05-K18.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION      library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
                HD--05-K18, mRNA sequence.

```

```

ACCESSION
VERSION         CF315940
KEYWORDS        CF315940.1 GI:33687701
SOURCE          EST.

```

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

```

```

REFERENCE
AUTHORS         Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
                Contact: Nahm B.H.

```

```

TITLE
JOURNAL         Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT         of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

FEATURES
source          Location/Qualifiers
                1..19

```

```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--05-K18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

```

ORIGIN

```

Query Match      42.1%; Score 8; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 CTCCTTCA 18
        |||||
        18 CTCCTTCA 11

```

```

RESULT 12
CF337272/c      19 bp      mRNA      linear      EST 18-AUG-2003
LOCUS           JMT--07-K10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION      library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
                JMT--07-K10, mRNA sequence.

```

```

ACCESSION
VERSION         CF337272
KEYWORDS        CF337272.1 GI:33822933
SOURCE          EST.

```

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BAP
clade; Ehrhartoideae; Oryzae; Oryza.

```

```

REFERENCE
AUTHORS         Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
                Contact: Nahm B.H.

```

```

TITLE
JOURNAL         Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT         of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

FEATURES
source          Location/Qualifiers
                1..19

```

```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-K10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

```

ORIGIN

```

Query Match      42.1%; Score 8; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 CTCCTTCA 18
        |||||
        11 CTCCTTCA 4

```

```

RESULT 13
AZ506614/c      19 bp      DNA      linear      GSS 05-OCT-2000
LOCUS           1M0347A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0347A24 R, genomic survey sequence.

```

```

ACCESSION
VERSION         AZ506614
KEYWORDS        AZ506614.1 GI:10687930
SOURCE          GSS.

```

ORGANISM

```

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,

```

TITLE
JOURNAL
COMMENT

Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Rally, M., Rose, R., Stokes, R., Tingey, A., von
Nederhausen, A. and Wright, D., Weiser, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiser
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0347 row: A column: 24
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0347A24"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCLM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 42.1%; Score 8; DB 11; Length 19;
Best Local Similarity 68.8%; Pred. No. 2.7e+07;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CACGATATCTCTTCA 18
||| ||| ||| ||| |||
Db 18 CACTGTCTCCATTTA 3

RESULT 14
A2995903 19 bp DNA linear GSS 27-APR-2001
LOCUS
DEFINITION 2M0281H19 Mouse 10kb plasmid UGCLM library mus musculus genomic
clone UGCLM0281H19 R, genomic survey sequence.
ACCESSION
VERSION A2995903
KEYWORDS A2995903.1 GI:13867130
SOURCE
ORGANISM Mus musculus (house mouse)
Buxarjota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Rally, M., Rose, R., Stokes, R., Tingey, A., von
Nederhausen, A. and Wright, D., Weiser, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiser
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0281 row: H column: 19
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0281H19"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCLM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 42.1%; Score 8; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ATCTCCTT 16
|||||
Db 5 ATCTCCTT 12

RESULT 15
CL657608 19 bp DNA linear GSS 09-JUL-2004
LOCUS
DEFINITION PRI012a.B12 - PRI012a.B21 (19) Note: Recurring String Mixed Stage
fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION
VERSION CL657608
KEYWORDS CL657608.1 GI:50139393
SOURCE
ORGANISM Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.


```

REFERENCE 1 (bases 1 to 19)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppABD: an AceDB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED 14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
    source
        1..19
            /organism="Pristionchus pacificus"
            /mol_type="genomic DNA"
            /strain="California"
            /db_xref="taxon:54126"
            /clone_lib="Mixed stage fosmid library of P. pacificus
            var. California"
            /note="Vector: pGiflow-5 Fosmid vector"
ORIGIN
Query Match 42.1%; Score 8; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 TCTCCTTC 17
Db 7 TCTCCTTC 14
RESULT 16
AJ587912 19 bp DNA linear GSS 15-JAN-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
339D06, genomic survey sequence.
ACCESSION AJ587912
VERSION AJ587912.1 GI:37937536
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE 1
AUTHORS Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G.,
Lepointec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
COMMENT 2 (bases 1 to 19)
Balzerque,S.
Direct Submision
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genopiante' (http://www.genopiante.com and

```

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http://genopiante-info.infobiogen.fr.
FEATURES
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            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /db_xref="taxon:3702"
            /clone="339D06"
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            left border"
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        left border"
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Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 ATCTCCTT 16
Db 8 ATCTCCTT 15
RESULT 17
AJ600880 19 bp DNA linear GSS 15-JAN-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone
515R04, genomic survey sequence.
ACCESSION AJ600880
VERSION AJ600880.1 GI:37950508
KEYWORDS GSS; right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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REFERENCE 1
AUTHORS Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G.,
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TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
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Balzerque,S.
Direct Submision
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
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derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genopiante' (http://www.genopiante.com and
http://genopiante-info.infobiogen.fr).
FEATURES
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        1..19
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            right border"
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 Best Local Similarity 68.8%; Pred. No. 2.7e+07;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 CACGGATTCCTTCA 18
 |||||
 3 CACGGATTAATTCTGA 18

Db

RESULT 18
 AZ308865/c 19 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0012M14F Mouse 10kb plasmid UGCLM library Mus musculus genomic
 DEFINITION clone UGCLM0012M14 F, genomic survey sequence.
 AZ308865
 ACCESSION AZ308865.1 GI:10349284
 VERSION GSS.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0012 row: M column: 14
 Seq primer: CGTTGTAAACGACGGCCACT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
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 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCLM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 41.1%; Score 7.8; DB 11; Length 19;
 Best Local Similarity 81.8%; Pred. No. 3.5e+07;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 ACGGATTCCTC 14
 |||||
 16 AAGGTAATCTCC 6

Db

RESULT 19
 AZ313113/c 19 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0029N17F Mouse 10kb plasmid UGCLM library Mus musculus genomic
 DEFINITION clone UGCLM0029N17 F, genomic survey sequence.
 AZ313113
 ACCESSION AZ313113.1 GI:10357719
 VERSION GSS.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0029 row: N column: 17
 Seq primer: CGTTGTAAACGACGGCCACT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
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1..19
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 /organism="Mus musculus"
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 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCLM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 41.1%; Score 7.8; DB 11; Length 19;
 Best Local Similarity 81.8%; Pred. No. 3.5e+07;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 ACGGATCTCC 14
 |||
 19 ACAGATCTCC 9

RESULT 20
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 LOCUS 1M0185P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0185P01 F, genomic survey sequence.
 ACCESSION AZ411858
 VERSION AZ411858.1 GI:10535871
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0185 row: P column: 01
 Seg primer: CCGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /strain="C57BL/6J"
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 /clone="UUGC1M0185P01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells

ORIGIN

Query Match 41.1%; Score 7.8; DB 11; Length 19;
 Best Local Similarity 81.8%; Pred. No. 3.5e+07;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 GGTATCTCCTT 16
 |||
 16 GGTTCCTATT 6

RESULT 21
 AZ514774 19 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M061M11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0361N11 R, genomic survey sequence.
 ACCESSION AZ514774
 VERSION AZ514774.1 GI:10696090
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0361 row: N column: 11
 Seg primer: CACACGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
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 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
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ORIGIN

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 41.1%; Score 7.8; DB 11; Length 19;
Best Local Similarity 81.8%; Pred. No. 3.5e+07;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 7 GATATCTCTTC 17
| | | | | | | | | |
Db 3 GTTCTACTTC 13

RESULT 22
AZ585898 19 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
clone UUGC1M0391L22 F, genomic survey sequence.
ACCESSION
AZ585898
VERSION
KEYWORDS
GSS.
GI:11708086

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0391 row: 1. column: 22
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Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
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adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
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purified. The sheared, adaptored mouse DNA was annealed to

ORIGIN

adaptored vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 41.1%; Score 7.8; DB 11; Length 19;
Best Local Similarity 81.8%; Pred. No. 3.5e+07;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 7 GATATCTCTTC 17
| | | | | | | | | |
Db 3 GCATCTACTTC 13

RESULT 23
AZ643528/c 19 bp DNA linear GSS 14-DEC-2000
LOCUS
DEFINITION
clone UUGC1M0507H05 F, genomic survey sequence.
ACCESSION
AZ643528
VERSION
KEYWORDS
GSS.
GI:11771193

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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REFERENCE
AUTHORS
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JOURNAL
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Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0507 row: H column: 05
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0507H05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
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Laboratory Mouse DNA Resource
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purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 41.1%; Score 7.8; DB 11; Length 19;
Best Local Similarity 63.2%; Pred. No. 3.5e+07;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTCAC 19
Db 19 CCAGCATCTCTTCTC 1

RESULT 24
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LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 292A05, genomic survey sequence.

ACCESSION AJ587549
VERSION AJ587549.1 GI:37937173
KEYWORDS GSS: left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE 1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Crnaud, C., Dreose, R., Pelletier, G., Lepoint, L., Caboche, M., and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)

REFERENCE 2 (bases 1 to 19)

Balzerque, S.

Direct Submision

Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).
Location/Qualifiers

FEATURES

source

1..19
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="292A05"
/clone_1ib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Massiliaewiki4"
1..19
/note="T-DNA flanking sequence
left border"

ORIGIN

Query Match 41.1%; Score 7.8; DB 14; Length 19;
Best Local Similarity 81.8%; Pred. No. 3.5e+07;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 ATCTCTTCTC 19
Db 4 ATCTCTTCTC 14

RESULT 25
CF281537/c 19 bp mRNA linear EST 14-AUG-2003
LOCUS 14ETL--08-K01.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa [japonica cultivar-group] cDNA clone 14ETL--08-K01, mRNA sequence.

ACCESSION CF281537
VERSION CF281537
KEYWORDS EST

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE 1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--08-K01"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1ib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

source

Query Match 40.0%; Score 7.6; DB 5; Length 19;
Best Local Similarity 71.4%; Pred. No. 4.5e+07;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTTC 14
Db 14 CGCTCGGCTTCTGC 1

RESULT 26
DR026632 19 bp mRNA linear EST 26-MAY-2005
LOCUS DR026632/c
DEFINITION Osmo01180 F. cylindrus osmotic stress library Fragilariopsis cylindrus cDNA clone Fcyl1ESTa42b03.g1, mRNA sequence.

ACCESSION DR026632
VERSION DR026632.1 GI:66748995

KEYWORDS EST

SOURCE Fragilariopsis cylindrus

ORGANISM Fragilariopsis cylindrus

REFERENCE 1 (bases 1 to 19)
Krell, A. and Gloeckner, G.
Analysis of an osmotic stress induced cDNA library of the psychrophilic diatom Fragilariopsis cylindrus

Unpublished (2004)

Contact: Krell, Andreas; Gloeckner, Gernot

Biological Oceanography, Sea Ice Research; Genome Analysis

Alfred-Wegener-Institute for Polar and Marine Research, Institute

COMMENT

JOURNAL

for Molecular Biotechnology
Am Handelshafen 12, D-27570 Bremerhaven, Germany; Beutenbergstr.
11, D-07745 Jena, Germany

Tel: +49 471 48311812; +49 3641 656440
Fax: +49 471 48311425; +49 3641 656255
Email: akrell@awi-bremerhaven.de; gernot@imb-jena.de

PCR primers

FORWARD: 5'M13

BACKWARD: 3'M13

Seq primer: 5'GTAAACGACGCCAG 3'

FEATURES

source

Location/Qualifiers

1..19 /organism="Fragilariopsis cylindrus"

/mol_type="rRNA"

/db_xref="taxon:186039"

/clone="FCylBESTa42b03.81"

/note="lib=F. cylindrus osmotic stress library"

/clone="Samples for total RNA isolation were taken

continuous for 5 days after a salt shock treatment

increasing salinity from 34 to 60 PSU. Total RNA

extraction was performed with RNeasy (Ambion) and mRNA

purification with polyA Purist (Ambion). Further steps

were carried out as described in the Cloneminer Kit. cDNA

size fractionation was carried out with CHROMA Spin-400

columns and additionally on a gel."

ORIGIN

Query Match

Best Local Similarity 40.0%; Score 7.6; DB 9; Length 19;

Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

4 ACAGTATCTCTTC 17

15 AGGTTCTTTTC 2

Db

RESULT 27

AZ314603

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

19 bp DNA linear GSS 29-SEP-2000

1M0031C06R Mouse 10kb plasmid UGCLM library Mus musculus genomic

clone UGCLM0031C06 R, genomic survey sequence.

AZ314603

1 GI:1036057

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Rilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weis

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

/mol_type="genomic DNA"

/accession="U031C06"

/db_xref="taxon:10090"

/clone="UGCLM0031C06"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g14732114|gb|AF12972.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match

Best Local Similarity 40.0%; Score 7.6; DB 11; Length 19;

Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

3 CACGATCTCTCTT 16

6 CAATGATCGCCTT 19

Db

RESULT 28

AZ505490

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

19 bp DNA linear GSS 05-OCT-2000

1M0346N08F Mouse 10kb plasmid UGCLM library Mus musculus genomic

clone UGCLM0346N08 F, genomic survey sequence.

AZ505490

1 GI:10686806

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Rilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weis

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0346 Row: N Column: 08

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/accession="U031C06"

/db_xref="taxon:10090"

/clone="UGCLM0031C06"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g14732114|gb|AF12972.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/accession="U031C06"

/db_xref="taxon:10090"

/clone="UGCLM0031C06"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g14732114|gb|AF12972.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Location/Qualifiers

1..19

/organism="Mus musculus"

```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0346N08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/notes="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```

Query Match      40.0%; Score 7.6; DB 11; Length 19;
Best Local Similarity 71.4%; Pred. No. 4.5e+07;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY      3 CACGGTATCTCCTT 16
        ||| ||| ||| |||
Db      6 GACCTCTCCTCCTT 19

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```

RESULT 29
AZS82154      19 bp      DNA      linear      GSS 13-DEC-2000
LOCUS      1M0374C19F Mouse 10kb plasmid UGGCM library Mus musculus genomic
DEFINITION      clone UGGCM0374C19 F, genomic survey sequence.
ACCESSION      AZS82154
VERSION      AZS82154.1 GI:11700755
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0374 row: C column: 19
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

```

```

REFERENCE
AUTHORS
JOURNAL
COMMENT

```

FEATURES

source

```

1.19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0374C19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/notes="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```

Query Match      40.0%; Score 7.6; DB 11; Length 19;
Best Local Similarity 71.4%; Pred. No. 4.5e+07;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY      3 CACGGTATCTCCTT 16
        ||| ||| ||| |||
Db      5 CGCGCTACTCCTT 18

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RESULT 30
AZ827164      19 bp      DNA      linear      GSS 20-FEB-2001
LOCUS      2M0103M22F Mouse 10kb plasmid UGGCM library Mus musculus genomic
DEFINITION      clone UGGCM0103M22 F, genomic survey sequence.
ACCESSION      AZ827164
VERSION      AZ827164.1 GI:1297072
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0103 row: M column: 22
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

```

```

REFERENCE
AUTHORS
JOURNAL
COMMENT

```

FEATURES

ORIGIN

Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: NYBG accession number #436/84"

Query Match 38.9%; Score 7.4; DB 9; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.7e+07;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 ATCTCCTC 17
|||||
6 ATCTTCTC 14

RESULT 33
AZ329293 19 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION 1M0053A03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0053A03 R, genomic survey sequence.

ACCESSION AZ329293
VERSION AZ329293.1 GI:10389864
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0053 row: A column: 03
Seq primer: CACACGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1. 19
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0053A03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

ORIGIN

purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 38.9%; Score 7.4; DB 11; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.7e+07;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TCTCCTTA 18
|||||
7 TCTCCATCA 15

RESULT 34
AZ443948 19 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION 1M0238P04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0238P04 F, genomic survey sequence.

ACCESSION AZ443948
VERSION AZ443948.1 GI:10592384
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0238 row: P column: 04
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1. 19
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0238P04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 38.9%; Score 7.4; DB 11; Length 19;
Best Local Similarity 64.7%; Pred. No. 5.7e+07;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 CACGGTATCTCTCTCAC 19
1 CCCCTGTCTCTCTCTC 17

Db

RESULT 35

AZ484016 19 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0310J10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0310J10 F, genomic survey sequence.

ACCESSION AZ484016
VERSION AZ484016.1 GI:10648549
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0310 row: J column: 10

Seq primer: CGTTGTAACGACGCCACT
Class: plasmid ends

High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0310J10"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 38.9%; Score 7.4; DB 11; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.7e+07;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TCTCCTCA 18
10 TTCTCTCA 18

Db

RESULT 36

AZ500675 19 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0339J10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0339J10 F, genomic survey sequence.

ACCESSION AZ500675
VERSION AZ500675.1 GI:10680728
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0339 row: J column: 10

Seq primer: CGTTGTAACGACGCCACT
Class: plasmid ends

High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0339J10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 38.9%; Score 7.4; DB 11; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.7e+07;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 CTCCTTCAC 19
16 CTCCTACAC 8

RESULT 37
AZ834038 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0116H01R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCM0116H01 R, genomic survey sequence.
ACCESSION AZ834038
VERSION AZ834038.1 GI:13003946
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D. Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genome.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 016 Row: H Column: 01
Seq primer: CACACAGGAACGCTATGACC
Class: Plasmid ends
High quality sequence stop: 19.

FEATURES
source
1.19 Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCM0116H01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 38.9%; Score 7.4; DB 11; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.7e+07;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 ATCTCTTC 17
13 ATCTCTTC 5

RESULT 38
AJ597721/c 19 bp DNA linear GSS 15-JAN-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 455F11, genomic survey sequence.
ACCESSION AJ597721
VERSION AJ597721.1 GI:37947349
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechold, N., Cruaud, C., Dekose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.

TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
COMMENT 12446565
2 (bases 1 to 19)
Balzerque, S.

REFERENCE
AUTHORS Direct Submission
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'genoplante' (<http://www.genoplante.com> and <http://genoplante-info.inbioigen.fr>).

FEATURES
source
1.19 Location/Qualifiers

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="455F11"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
1.19 "T-DNA flanking sequence
left border"

ORIGIN

Query Match 38.9%; Score 7.4; DB 14; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.7e+07;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTT 16
 |||||
 Db 19 TAGCTCCTT 11

RESULT 39
 AM075504/c
 LOCUS
 DEFINITION AM075504 Chicken immune 5 - CSEQRBN30 Gallus gallus CDNA clone

AM075504 19 bp mRNA linear EST 14-SEP-2005
 AM075504 C0000798016_T7, mRNA sequence.
 AM075504
 AM075504.1 GI:75476089
 EST.
 Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 19)
 Smith, J., Speed, D., Hocking, P., Talbot, R.T., Degen, W., Schijne, V.,
 Glass, E.J. and Burt, D.
 Development of a chicken 5k array
 Unpublished (2005)
 TITLE
 JOURNAL
 COMMENT
 Genetics and Genomics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Vector pBluescript II KS(+) R. Site1: EcoRI R. Site2: NotI 5' Seg
 Primer T7 Strain Lohman Brown layer/Rose 308 broiler cross This
 normalized library was constructed from 1 million independent
 clones. cDNA synthesis was initiated using an oligo(dT) primer,
 using methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA was
 blunt-ended, ligated to NotI adapters, digested with EcoRI,
 size-selected, and cloned into the NotI and EcoRI compatible sites
 of a custom modified MCS of the pBluescript (KS+) vector. The
 library was normalized in 2 rounds using conditions adapted from
 Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome
 Research 6 (1996): 791, except that a significantly longer
 reannealing hybridization was used. Clones available from the
 ARK-Genomics Centre for Functional Genomics in Farm Animals, Roslin
 Institute, Midlothian, EH25 9PS, UK see www.ark-genomics.org.
 Location/Qualifiers
 1..19
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="C0000798016_T7"
 /issue_type="thymus"
 /clone_lib="Chicken immune 5 - CSEQRBN30"

ORIGIN

Query Match 37.9%; Score 7.2; DB 1; Length 19;
 Best Local Similarity 75.0%; Pred. No. 7.3e+07;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CACGCTATCTCC 14
 |||||
 Db 12 CGCGGAGACTCC 1

RESULT 40
 BX560116/c
 LOCUS
 DEFINITION BX560116 Glossina morsitans morsitans adult infected gut Glossina
 morsitans morsitans CDNA clone Tse48a12_glc, mRNA sequence.
 BX560116
 BX560116.1 GI:33368195
 EST.
 Glossina morsitans morsitans
 Glossina morsitans morsitans
 Eukaryota; Metazoa; Archiroptera; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 COMMENT
 14519198
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix glc are reverse primer reads starting at 5'
 end of the cDNA all pic reads are from
 the 3' end.
 Location/Qualifiers
 1..19
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse48a12_glc"
 /issue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T. brucei"

ORIGIN

Query Match 37.9%; Score 7.2; DB 4; Length 19;
 Best Local Similarity 75.0%; Pred. No. 7.3e+07;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCAAGGTATCTC 13
 |||||
 Db 17 GCAAGGTATCTC 6

Search completed: August 10, 2006, 11:03:01
 Job time: 1861.67 secs

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